

STIC-Biot ch/Ch mLib

61492

From: Pak, Michael
Sent: Friday, March 01, 2002 8:59 AM
To: STIC-Biotech/ChemLib
Subject: 09/276,935 sequence search

Sequence search - 2 month amendment
App. #: 09/276,935
Result format: Paper.
Title: an orphan nuclear receptor

Please search:

Search commercial and interference database.

SEQ ID NO: 13-14

Edward Han
Technical Info. Specialist
STIC/Biotech
Tel 305-9203

Thanks,

Mike Pak

Michael Pak
Art Unit 1646
Mailbox: CM1, Rm. 10C00
Office: CM1, Rm. 10E13
703-305-7038

Michael Pak
USPTO
Art Unit 1646
CM1, Rm. 10E13
703-305-7038

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 3/1/02
Date Completed: 3/2/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 64
WWW/Internet: _____
Other (specify): _____

Genotex version 4.5
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OM protein - protein search, using sw model

Run on: March 2, 2002, 01:50:25 ; Search time 22.59 seconds
(without alignments)
412.411 Million cell updates/sec

Title: US-09-276-935b-14

Percent score: 2187
Sequence: 1 LEVAPKESMNAHAPVCHCEDI.....AMTEFAPIMLKELITICS 414

Scoring table:
BLAST/OM62
Gapop 10.0 ; Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 9%
Maximum Match 100%

Library Title: 45 summaries

Database :

1: Issued Patents AA:
2: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	750	34.3	427	4	US-08-764-870-11 Sequence 11, Appl
2	741	33.4	448	1	US-08-459-489-10 Sequence 10, Appl
3	741	33.4	448	1	US-08-458-686-10 Sequence 10, Appl
4	731	33.4	448	1	US-07-843-350C-10 Sequence 10, Appl
5	590	27.0	367	1	US-07-737-736B-4 Sequence 4, Appl
6	472	21.6	461	1	US-08-430-518-2 Sequence 2, Appl
7	472	21.6	461	1	US-08-430-283-2 Sequence 2, Appl
8	472	21.6	461	1	US-08-646-248-2 Sequence 2, Appl
9	472	21.6	461	5	PCT-US95-13924-2 Sequence 2, Appl
10	472	21.6	461	5	PCT-US95-13924-2 Sequence 2, Appl
11	470	21.5	460	1	US-08-342-411A-2 Sequence 2, Appl
12	464	21.2	446	2	US-08-372-652-3 Sequence 3, Appl
13	464	21.2	446	5	PCT-US95-16411-3 Sequence 3, Appl
14	461	21.1	444	4	US-08-776-844-2 Sequence 2, Appl
15	457	20.9	444	1	US-08-442-411A-4 Sequence 4, Appl
16	456.5	20.9	440	1	US-08-333-358-8 Sequence 8, Appl
17	456.5	20.9	440	1	US-08-463-694-8 Sequence 8, Appl
18	456.5	20.9	440	1	US-08-694-501-8 Sequence 8, Appl
19	456.5	20.9	442	1	US-08-373-935-1 Sequence 1, Appl
20	424.5	19.4	477	1	US-08-496-631-2 Sequence 2, Appl
21	424	19.3	461	4	US-08-764-870-3 Sequence 3, Appl
22	424	19.3	461	4	US-08-980-115-3 Sequence 3, Appl
23	410	18.7	455	6	5223606-4 Patent No. 5223606
24	409	18.7	469	3	US-08-472-183-2 Sequence 2, Appl
25	409	18.7	469	3	US-09-469-721-2 Sequence 2, Appl
26	409	18.7	469	5	PCT-US95-17023-2 Sequence 2, Appl
27	406.5	18.6	484	2	US-08-372-652-1 Sequence 1, Appl

28	406.5	18.6	484	5	PCT-US95-16311-1 Sequence 1, Appl
29	405.5	18.5	746	3	US-09-144-759-18 Sequence 18, Appl
30	405.5	18.5	764	3	US-09-144-759-20 Sequence 20, Appl
31	399.5	18.3	451	2	US-08-372-652-2 Sequence 2, Appl
32	399.5	18.3	451	5	PCT-US95-16411-2 Sequence 2, Appl
33	394	18.0	410	4	US-08-764-870-2 Sequence 2, Appl
34	394	18.0	410	4	US-08-980-115-2 Sequence 2, Appl
35	394	18.0	410	6	5438126-2 Patent No. 5438126
36	390	17.8	410	4	US-08-764-870-1 Sequence 1, Appl
37	390	17.8	410	4	US-08-980-115-1 Sequence 1, Appl
38	388	17.7	606	4	US-08-891-298-3 Sequence 3, Appl
39	387	17.7	448	6	5223606-2 Patent No. 5223606
40	379.5	17.4	433	2	US-08-466-120-2 Sequence 2, Appl
41	379.5	17.4	433	5	PCT-US94-07266-2 Sequence 2, Appl
42	372	17.0	462	2	US-08-592-484-2 Sequence 2, Appl
43	372	17.0	462	2	US-08-095-728B-4 Sequence 4, Appl
44	372	17.0	462	5	PCT-US92-02320A-4 Sequence 4, Appl
45	372	17.0	797	2	US-08-095-728B-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-764-870-11
Sequence 11, Application US/08764870
Patent No. 6246946
GENERAL INFORMATION:
APPLICANT: Scantien, Thomas S
APPLICANT: Baxter, John D
APPLICANT: Fletcher, Robert J
APPLICANT: Wagner, Richard L
APPLICANT: Kushner, Peter J
APPLICANT: Appleton, James W
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
TITLE OF INVENTION: Binding Domains
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Cooley Goddard
STREET: Five Palo Alto Square, 4000 El Camino Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764-870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 540
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/EXCERPT NUMBER: JPAT-246/0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid

1 SUPPLEMENTARY:
2 Type: 11000
3 Model: 11000
4 OS: 00 704 870 11

5 Query Match: 64.58% Score: 7502 DB: 4 Length: 4272

6 Best Local Similarity: 40.58% Prod. No: 1, 90, 662

7 Matches: 1972 Conservative: 622 Missed Chos: 1302 Indels: 402 Gaps: 62

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RESULT 2
US 08 459 489 10

1 Sequence ID: Application US/08459489
2 Patent No: 5666574
3 GENERAL INFORMATION:
4 APPLICANT: David D. Moore et al.
5 TITLE OF INVENTION: CAR RECEPTORS AND RELATED
6 NUMBER OF SEQUENCES: 10
7 CORRESPONDENT ADDRESS:
8 ADDRESS: Fish & Richardson
9 STREET: 275 Franklin Street
10 CITY: Boston
11 STATE: Massachusetts
12 COUNTRY: U.S.A.
13 ZIP: 02110 2804
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 4.5" Diskette, 1.44 MB
16 COMPILER: IBM PS/2 Model 502 of OSX
17 OPERATING SYSTEM: IBM P.C. DOS (Version 4.00)
18 SOFTWARE: WordPerfect (Version 5.0)
19 SUPPORT DATA DATA:
20 APPLICATION NUMBER: US/08/459,489
21 FILING DATE:
22 CLASSIFICATION: 455
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 07/844,450
25 FILING DATE: February 26, 1992
26 AGENT/AGENT INFORMATION:
27 NAME: Paul F. Clark
28 REGISTRATION NUMBER: 40,162
29 REFERENCE/JACKET NUMBER: 00786/126001
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (617) 542 5070

1 REFERENCE: (617) 542 8606
2 REFERENCE: 200154
3 INFORMATION FOR SEQ ID NO: 10:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 448
6 TYPE: amino acid
7 STRANDNESS: N/A
8 TOPOLOGY: linear
9 US 08 459 489 10

10 Query Match: 44.48% Score: 7411 DB: 1 Length: 448
11 Best Local Similarity: 40.58% Prod. No: 1 to 662
12 Matches: 1972 Conservative: 592 Missed Chos: 1002 Indels: 722 Gaps: 62

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RESULT 3

US 08 459 489 10

1 Sequence ID: Application US/08459489
2 Patent No: 5710017
3 GENERAL INFORMATION:
4 APPLICANT: David D. Moore et al.
5 TITLE OF INVENTION: CAR RECEPTORS AND RELATED
6 NUMBER OF SEQUENCES: 10
7 CORRESPONDENT ADDRESS:
8 ADDRESS: Fish & Richardson
9 STREET: 275 Franklin Street
10 CITY: Boston
11 STATE: Massachusetts
12 COUNTRY: U.S.A.
13 ZIP: 02110 2804
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 4.5" Diskette, 1.44 MB
16 COMPILER: IBM PS/2 Model 502 of OSX
17 OPERATING SYSTEM: IBM P.C. DOS (Version 4.00)
18 SOFTWARE: WordPerfect (Version 5.0)
19 SUPPORT DATA DATA:
20 APPLICATION NUMBER: US/08/459,489
21 FILING DATE:
22 CLASSIFICATION: 514
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 07/844,450
25 FILING DATE: February 26, 1992
26 AGENT/AGENT INFORMATION:
27 TELEPHONE: (617) 542 5070

NAME: Paul T. Clark
 REGISTRATION NUMBER: 40,162
 REFERENCE/DOCKET NUMBER: 00786/126001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: linear
 US-08-458-686-10

Query Match 44.4%; Score 731; DB 1; Length 448;
 Best Local Similarity 40.5%; Pred. No. 1,1e-64;
 Matches 157; Conservative 59; Mismatches 100; Indels 72; Gaps 6;

QY 41 CAVGCDKATGYHFNMTTCCKGFFRRAMKRNALRCFRRKACGLTTRKTRGCGACLR 100
 DB 11 CAVGCDATGYHFNMTTCCKGFFRRATVSKSGTPCF-AGSCVSKTORRHHPACGLQ 69
 QY 101 KCLSGMKKEMIMSDAVERRALIKRKSFRGTGTPGVGLTEPQMMKEIMDAQK 160
 DB 70 KCLDAMKMDMLISALALAKRAKQAKRAQDTVY-----LSKEQELLITLLGANTK 123
 QY 161 TFDTFSHKRNRLPGVLSGCELPESLQAPSRFEAKMSQVRKDLSTKVSLOLGEDG 220
 DB 124 HMTTFEFGVQFRRPHLEIHQ-PLPTIAP----- 153
 QY 221 SWNNKPPADSCKELFSLPHMAIMSTYMGKIIISFAKVISYFRLDPLEIDISLKGA 280
 DB 154 -----VLPVTFADINTFMVLQVTKFDLPVFRSLPLEIDISLKGA 198
 QY 281 FELQLRNTVNAETGCGWENGLSYGLDPTAG-GFQQLLEPMKPHYMLKQLDHEE 339
 DB 199 VEGCHIVLNTFGDTQNTLCQPLRTYTDGAKVQVQVHLELPHRFGTLKRLQDDE 258
 QY 340 YVIMQALISLSPDRGVIGHRVVDLOEUFATIKSYLPCNRPQAHREPLKIMAMTE 399
 DB 259 YVILAAALFSPDRGVIGDRDELDOLEEMALTIQSYIKQDRPRDRFLVAKLIGLAE 318
 QY 400 FAT-----PIMQEL 408
 DB 319 LRSINEAVGYDTIGLSAMMPLLOET 346

RESULT 4
 US-07-843-350C-10
 Sequence 10, Application US/07843350C
 Patent No. 5766448
 GENERAL INFORMATION:
 APPLICANT: David D. Moore et al.
 TITLE OF INVENTION: GAB RECEPTORS AND RELATED
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 555X
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 SOFTWARE: WordPerfect (Version 5.0)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/843,350C
 FILING DATE: February 26, 1992

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 40,162
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: linear
 US-07-843-350C-10

Query Match 33.4%; Score 731; DB 1; Length 448;
 Best Local Similarity 40.5%; Pred. No. 1,1e-64;
 Matches 157; Conservative 59; Mismatches 100; Indels 72; Gaps 6;

QY 41 CAVGCDKATGYHFNMTTCCKGFFRRAMKRNALRCFRRKACGLTTRKTRGCGACLR 100
 DB 11 CAVGCDATGYHFNMTTCCKGFFRRATVSKSGTPCF-AGSCVSKTORRHHPACGLQ 69
 QY 101 KCLSGMKKEMIMSDAVERRALIKRKSFRGTGTPGVGLTEPQMMKEIMDAQK 160
 DB 70 KCLDAMKMDMLISALALAKRAKQAKRAQDTVY-----LSKEQELLITLLGANTK 123
 QY 161 TFDTFSHKRNRLPGVLSGCELPESLQAPSRFEAKMSQVRKDLSTKVSLOLGEDG 220
 DB 124 HMTTFEFGVQFRRPHLEIHQ-PLPTIAP----- 153
 QY 221 SWNNKPPADSCKELFSLPHMAIMSTYMGKIIISFAKVISYFRLDPLEIDISLKGA 280
 DB 154 -----VLPVTFADINTFMVLQVTKFDLPVFRSLPLEIDISLKGA 198
 QY 281 FELQLRNTVNAETGCGWENGLSYGLDPTAG-GFQQLLEPMKPHYMLKQLDHEE 339
 DB 199 VEGCHIVLNTFGDTQNTLCQPLRTYTDGAKVQVQVHLELPHRFGTLKRLQDDE 258
 QY 340 YVIMQALISLSPDRGVIGHRVVDLOEUFATIKSYLPCNRPQAHREPLKIMAMTE 399
 DB 259 YVILAAALFSPDRGVIGDRDELDOLEEMALTIQSYIKQDRPRDRFLVAKLIGLAE 318
 QY 400 FAT-----PIMQEL 408
 DB 319 LRSINEAVGYDTIGLSAMMPLLOET 346

RESULT 5
 US-07-737-736R-4
 Sequence 4, Application US/07737736R
 Patent No. 5260199
 GENERAL INFORMATION:
 APPLICANT: Delella, Hector F.
 APPLICANT: Ross, Troy K.
 APPLICANT: Prabh, Jeon M.
 TITLE OF INVENTION: Method of Producing
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carl R. Schwartz, Esq., c/o Charles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53202
 COMPUTER READABLE FORM:

1 MEDIA/TYPE: floppy disk
 2 COMMENT: IBM pc compatible
 3 OPERATING SYSTEM: pc bios/ms dos
 4 SOFTWARE: Pattern Bios #1.0, Version #1.25
 5 INFORMATION: Pattern Bios
 6 APPLICATION NUMBER: US/073737.1 (668
 7 FILING DATE: 19910730
 8 CLASSIFICATION: 435
 9 ALLOCNRY/AGENCY INFORMATION:
 10 NAME: Schwartz, Carl R.
 11 PERSISTENCE NUMBER: 29,434
 12 REFERENCE/PROJECT NUMBER: 96 296 2185, 2
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: 414 277 5115
 15 TELEFAX: 414 277 5174
 16 INFORMATION FOR SEQ ID NO: 4:
 17 SEQUENCE CHARACTERISTICS:
 18 LENGTH: 667 amino acids
 19 TYPE: AMINO ACID
 20 STRANDEDNESS: single
 21 TOPOLOGY: linear
 22 FEATURE TYPE: protein
 23 HYDROPHILIC: No
 24 ANTI SENSE: No
 25 ORIGIN: Source:
 26 ORGANISM: Rat
 27 ORGANISM INFORMATION:
 28 AUTHORITY: Burnstock, James R.
 29 AUTHORITY: Miesch, No. 52619990
 30 AUTHORITY: DeLacy, Hector F.
 31 TITLE: Isolation and expression of rat
 32 TITLE: 1,25-dihydroxyvitamin D₃ receptor cDNA
 33 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 34 VOLUME: 85
 35 PAGES: 1005-1009
 36 DATE: February 1988
 37 DB ID: 147 7466 4

Order	Material	Weight, g	Length, mm	Width, mm	Thickness, mm	Volume, cm ³	Mass, g	Density, g/cm ³
1	Aluminum	10.0	100.0	10.0	1.0	10.0	10.0	2.70
2	Steel	10.0	100.0	10.0	1.0	10.0	10.0	7.85
3	Brass	10.0	100.0	10.0	1.0	10.0	10.0	8.50
4	Copper	10.0	100.0	10.0	1.0	10.0	10.0	8.96
5	Iron	10.0	100.0	10.0	1.0	10.0	10.0	7.87
6	Lead	10.0	100.0	10.0	1.0	10.0	10.0	11.35
7	Mercury	10.0	100.0	10.0	1.0	10.0	10.0	13.6
8	Water	10.0	100.0	10.0	1.0	10.0	10.0	1.0
9	Oil	10.0	100.0	10.0	1.0	10.0	10.0	0.9
10	Gas	10.0	100.0	10.0	1.0	10.0	10.0	0.001

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US 08 440 518 2
Sequence 2: Application US/08440518
Patient No.: 5607667
GENERAL INFORMATION:
Applicant : Fiedman, Etlan
Applicant : Holmway, M. Kathleen
Applicant : Rodan, Gidon
Applicant : Schmidt, Arieel
Applicant : Vogel, Robert
TITLE OF INVENTION: USE OF REFLECTOR POTENTIATORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Metek & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILED BY: pc compaitlto
OPERATING SYSTEM: pc ios/ms dos
SOFTWARE: Patcon II Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08440518
FILING DATE:
CLASSIFICATION: 445
ALTERNATIVE INFORMATION:
NAME: Holmway, Kathleen A.
REGISTRATION NUMBER: 46,502
REFERENCE/PACKET NUMBER: 19416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594 4284
TELEFAX: (908) 594 4270
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRAND DENSES: Single
POLARITY: 1 to 461
MOLECULAR TYPE: Peptide
HYDROPHILIC: No
ANTI SENSE: No
US 08 440 518-2

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1	2187	100.0	414	20	AAV42691	Human preneane X
2	2167	59.1	434	20	AAV15931	A human intranuclei
3	2167	99.1	457	20	AAV16035	A human intranuclei
4	2167	99.1	457	20	AAV15932	A human intranuclei
5	2167	99.1	466	20	AAV25410	Human nNKT paria
6	2167	99.1	473	20	AAV25411	Human nNKT-1 prota
7	2167	99.1	473	20	AAV15936	A human intranuclei
8	2167	99.1	473	20	AAV15935	A human intranuclei
9	2167	99.1	473	20	AAV094516	Human vitamin D r
10	2165	94.0	437	20	AAV09515	Human vitamin D r
11	2049	93.7	434	20	AAV21799	Human steroid and

PS Claim 4; Fig 1A-1); 69pp; English

XX	FR	11-AUG-1997:	97JP-0230345.
XX	XX	(NLSB) JAPAN TOHAI CO. INC.	
XX	DR	WP1: 1999-350330/40.	
OR	NR	N-PDSH; AAX59975.	
XX	PI	New intranuclear receptor protein - useful for drug development and	
PI	diagnosis and treatment of disease		
XX	FS	Disclosure: Page 35-37; 48pp; Japanese.	
XX	PS		
CC	T	present sequence represents a human intranuclear receptor protein.	
CC	F	nucleic acid sequence was isolated from a human adult cDNA	
CC	I	library using a swedish ANU3 derived probe. The protein can	
CC	B	be used for the development of drugs and diagnosis and treatment	
CC	C	of various diseases.	
XX	SO	Sequence 457 AA;	
Query Match		99.1% Score 2167; DB 20; Length 457;	
Best Local Similarity		95.4% Pred. No. 69 207;	
Matches 414; Conservative 0; Mismatches 0; Indels 20; Gaps			
UY	1	LEVNKESSNNADPHVCHETESVPKPSVNADEFGDYGICRVGDKATGYHPNVTCGC	60
DB	24	LEVTPKSWHADTVHCDCVSPKKPVNADVEYGPQIFCVGQKATGYHTNMTCG	83
UY	61	CKGFRRAMKRARAKCTPPKACCTETRTKRCQCAGRLRKLTESGMKEMTMSDAVE	120
DB	84	CKGTFRAMKVARTCPTRKAACELTCTRGCQACTRKLCSGMKKMIMSDAVE	143
UY	121	KRALIKRRKSERTGQPLCYOGLTFEFOHKMIHEIMAAQKTEDTFESHKNPRLPGVLSS	180
DB	144	TRALKTKKSECTGQPLAVQQLTEQGIMITEIMDAQMLDLDTLSHKNIPLPVLS	203
UY	181	GCELPESTQAASREFAAWWSQVRKDLCISKVSLQIRGEFDSVMWVKPAISNGKETFLSI	240
DB	204	QEQLPESTQAPSRVADKSGYRKIDCSIKVSLQIRGEDSGSWNYKPPADSQKELTSIL	263
UY	241	PHMALMTVMYMKGISLFEKAVISYFEDLPLEHQISTLKGAPELCQIRENTVENAETGWME	300
DB	264	PHMASTMYMKGLISTAKVISYFEDLPLEHQISTLKGAPELCQIRENTVENAETGWME	323
UY	301	CGRLLSYCELDIAGGGQQULLLEPKLFHYMKKRLQHREEVYMQAISTSPDRGVLYQR	360
DB	424	CGRLSYCELDIAGGGQQULLLEPMKTHYLKTLQHEEYVLMQALISTPDPRVLYQR	383
UY	361	VNDQLQEDFPALITKSVYECNKRPQPHREFLEKIMAMITP-----F	400
DB	384	VNDQLQEDFATLITKSVYECNPGRPHRTITLKIMAMITCETSINAQHTQRIIRIGIHPT	443
UY	401	ATPEMDELGITGS	414
DB	444	ATPLMGQITGLTAS	457
RESULT	4		
ID	AAV15942		
XX	AAV15942	standard; Protein: 457 AA.	
AC	AAV15942;		
XX	XX		
DT	04-AUG-1999	(first entry)	
XX	XX	A human intranuclear receptor protein.	
DE	XX	Human: intranuclear receptor protein; drug development; diagnosis;	
XX	XX	treatment.	
XX	XX		
OS	XX	Human samples.	

XX	JP11127872-A	98JP-0224172.	99.1%	Score 2167;	DB 20;	Length 457;	
XX	18-MAY-1999.		95.4%	Pred. No. 60-207;	Indels 20;	Gaps 1;	
XX	07-AUG-1998;	98JP-0224172.	0;	Mismatches 0;	Indels 20;	Gaps 1;	
XX	11-AUG-1997;	97JP-0230335.					
XX	(NISH) JAPAN TOBACCO INC.						
XX	WPI: 1999-350300/80.						
XX	N-PSDB: AAX59667.						
XX	New intranuclear receptor protein - useful for drug development and						
XX	diagnosis and treatment of disease						
XX	Claim 2: Page 16-17; 38pp; Japanese.						
XX	The present sequence represents a human intranuclear receptor protein.						
XX	The nucleic acid sequence was isolated from a human adult cDNA						
XX	library using a swollish AN024 derived probe. The protein can						
XX	be used for the development of drugs and diagnosis and treatment						
XX	of various diseases.						
XX	Sequence 457 AA;						
XX	Query Match	99.1%	Score 2167;	DB 20;	Length 457;		
XX	Best Local Similarity	95.4%	Pred. No. 60-207;	Indels 20;	Gaps 1;		
XX	Matches 414; Conservative 0; Mismatches 0; Indels 20; Gaps 1;						
XX	1 LEVERESNMADPHECHETPESPKPSVNADEMGCHQICWQGDKAIQYHNMVCHS 60						
XX	24 Ievrpkewmhadrlhctectsvpkpsvnaecvqpficvqdkatqytnumcog 83						
XX	61 CKGFRRAMKRNNAKIKCPHKGACETIKTKRQYVACRLKCTESGKKEMTMSDAVEE 120						
XX	84 CKGFRRAMKRNNAKIKCPHKGACETIKTKRQYVACRLKCTESGKKEMTMSDAVEE 143						
XX	121 KRALIKRKKSEGTGPIGVQGLTFEGKMTIRLMAQKTEFTTFSHKNKRIKGVSS 180						
XX	144 IralIKRKKSEGTGPIGVQGLTFEGKMTIRLMAQKTEFTTFSHKNKRIKGVSS 203						
XX	181 GCELHESIQAPSRERAAKMSQVRKDCSLKVSJOLRGELGSWANKPRASNGKTEFTSL 240						
XX	204 GcelHESIQAPSRERAAKMSQVRKDCSLKVSJOLRGELGSWANKPRASNGKTEFTSL 263						
XX	241 PHMAIMSTYMKKQITSFPAKIVSFPRDPIELDILSLKGAPELQALRNTVNAETGWE 300						
XX	264 PHMAIMSTYMKKQITSFPAKIVSFPRDPIELDILSLKGAPELQALRNTVNAETGWE 323						
XX	301 CGRLSYCTLEDTAGCGVQQLLEPMIKFHYMLKRIQIHFFYVLMQALSLPSTKPRVQLDR 360						
XX	324 CGRLSYCTLEDTAGCGVQQLLEPMIKFHYMLKRIQIHFFYVLMQALSLPSTKPRVQLDR 383						
XX	361 VVDQIQGFATIKSYTECNTPQAHRTILIKIMAMTCTSTNADQCTITTPQGLDPT 420						
XX	384 VVDQIQGFATIKSYTECNTPQAHRTILIKIMAMTCTSTNADQCTITTPQGLDPT 443						
XX	401 ATPLMDELFGTGS 414						
XX	444 atplmgeltlqtgs 457						
XX	RESULT 5						
XX	AAV25410						
XX	AAV25410 standard; Protein: 406 AA.						
XX	AAV25410;						
XX	06-SEP-1999 (first entry)						


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UY 301 CGRLSYCLFPIAGFCOULLHEMLKFRHMLKKLQIHEHEVYLMGALSLFSPRPGVIGHR 360
DB 340 carlsyctedtaqqtqlllepmkthymkklqllheevylmgaistlsprpvgllqr 399
UY 361 VVDOLOEOPATILKSYIEGCRNPOAHRELFLKIMAMTE-----F 400
DB 400 vvdqllqetfaiitksyiecmppahrrlllkimamtelcstrlnaghtqrlrrlqdlhpt 459
UY 401 ATPMLQELPGITGS 414
DB 460 atplmqelptgts 474

RESULT 7
AAV15936
ID AAV15936 standard: Protein: 473 AA.
AC AAV15936;
XX
XX 04-AUG-1999 (first entry)
DE A human intranuclear receptor protein.
XX
XX Human: intranuclear receptor protein; drug development; diagnosis;
XX treatment.
XX
XX Homo sapiens:
XX JP11127872-A.
XX 18-MAY-1999.
XX
XX 07-AUG-1998; 98JP-0224172.
XX
XX 11-AUG-1997; 97JP-0230335.
XX
XX (NISH) JAPAN TOHACCO INC.
XX
XX WPI: 1999-350330/40.
XX
XX N-PSDB: AAX59974.
XX
XX New intranuclear receptor protein - useful for drug development and
XX diagnosis and treatment of disease.
XX
XX PS Disclosure: Page 32-35; 38pp; Japanese.
XX
XX CC The present sequence represents a human intranuclear receptor protein.
XX
XX CC The nucleic acid sequence was isolated from a human adult cDNA
XX library using a swollish AMO23 derived probe. The protein can
XX be used for the development of drugs and diagnosis and treatment
XX of various diseases.
XX
XX Sequence 473 AA:

Query Match 99.1%; Score 2167; DB 20; Length 473;
Best Local Similarity 95.4%; Pred. No. 6, 3e-207;
Matches 414; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

```

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DB 220 gceipstqasrecaakswqrtdicslksilqtrddqsvwykppadqujckstsl 279
UY 241 PHMADMTYMKKGIISFAKVISYFRDLPLEQISLKGAAHELOJLKNVENAFETQWE 300
DB 280 phmadmtymkkgiistakvisytrdpldqstllkkaatoleqjtnvthuetatwo 349
UY 301 CGRLSYCLFPIAGFCOULLHEMLKFRHMLKKLQIHEHEVYLMGALSLFSPRPGVIGHR 360
DB 340 carlsyctedtaqqtqlllepmkthymkklqllheevylmgaistlsprpvgllqr 399
UY 361 VVDOLOEOPATILKSYIEGCRNPOAHRELFLKIMAMTE-----F 400
DB 400 vvdqllqetfaiitksyiecmppahrrlllkimamtelcstrlnaghtqrlrrlqdlhpt 459
UY 401 ATPMLQELPGITGS 414
DB 460 atplmqelptgts 474

RESULT 8
AAV15943
ID AAV15943 standard: Protein: 473 AA.
AC AAV15943;
XX
XX 04-AUG-1999 (first entry)
DE A human intranuclear receptor protein.
XX
XX Human: intranuclear receptor protein; drug development; diagnosis;
XX treatment.
XX
XX Homo sapiens:
XX JP11127872-A.
XX 18-MAY-1999.
XX
XX 07-AUG-1998; 98JP-0224172.
XX
XX 11-AUG-1997; 97JP-0230335.
XX
XX (NISH) JAPAN TOHACCO INC.
XX
XX WPI: 1999-350330/40.
XX
XX N-PSDB: AAX59968.
XX
XX New intranuclear receptor protein - useful for drug development and
XX diagnosis and treatment of disease.
XX
XX PS Claim 2: Page 17-19; 38pp; Japanese.
XX
XX CC The present sequence represents a human intranuclear receptor protein.
XX
XX CC The nucleic acid sequence was isolated from a human adult cDNA
XX library using a swollish AMO23 derived probe. The protein can
XX be used for the development of drugs and diagnosis and treatment
XX of various diseases.
XX
XX Sequence 473 AA:

Query Match 99.1%; Score 2167; DB 20; Length 473;
Best Local Similarity 95.4%; Pred. No. 6, 4e-207;
Matches 414; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

```


PR 41-MAR-1998; 98SE-000114B.
PR 14-OCT-1997; 97SE-000374S.

PA (PHMA) PHARMACIA & UPJOHN AB.

P1 Berkovitsam A, Dahlberg M

WP1: 1999-102508/25

1)R N-PSIB; AAX56242.

PI New vitamin D receptor related (VDR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

PS Claim 19, Page 19-20; 35pp; English.

The present sequence is a human vitamin D receptor related (VDRR) polypeptide. Human VDRR polypeptides and substances which affect VDRR signal transduction, can be used for treating metabolic, proliferative or inflammatory conditions. They can be used in the manufacture of a medicament for treating the following conditions: obesity, diabetes, anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and malignant tumours, hyperproliferative skin disorders or hypertyrosidism. Nucleic acid vectors encoding for expression of a VDRR polypeptide can be used for treating metabolic, proliferative or inflammatory conditions by introducing them into a mammal. The introduced nucleic acid is then capable of transforming a cell in vivo and then polypeptide is expressed. A substance affecting VDRR signal transduction, such as an agonist or antagonist, can be used for the manufacture of a medicament for treating metabolic, proliferative or inflammatory condition.

N.B. The specification specifically claims the VDRR nucleic acid and polypeptide sequences given in Figures 1, 4, 7 and 8, but no figures are given in the specification.

Sequence 447 AA;

Query Match

Best Local Similarity	95.2%	pred. No. 8.9e-207
Matches	413	Conservativeness
	1	Mismatches
	0	Indels
	20	Gaps
	1	

```

0Y 1 LEVRKESWMIADIVHECDTESYGGKPSVNADEVGGOICRKGODKATGHNFWMTCEG 60
Db 1 mevrkswmiadivhecdtesypgkpsvnaadevggqicrvgqdkatgynfwmtceg 60
0Y 61 CKGFRRAMKRNARLRCFFRKAGACEITRTKTRGOACRLKGLCSGKKKEIMSDAVEE 120
Db 61 ckgfrramkrrnarlrccffrkagaceitrtktrgoacrlkglcsgkkkeimsdavee 120
0Y 121 RRAA:LRKRSFETGTOPAGVAGITFEEDRMRLREIMDAOMKTFOTFSHFKKRLDVLSS 180
Db 121 rraa:lrkrsfetgtopagvagitfeedrmrlreimdaomktfotfshfkkrldvls 180
0Y 121 rraa:lrkrsfetgtopagvagitfeeqmmmlreimdaomktdtllshkrltrpylss 180
Db 121 rraa:lrkrsfetgtopagvagitfeeqmmmlreimdaomktdtllshkrltrpylss 180
0Y 181 GGELEPESIOALSRKPAKWSOVRRKDI/SIKVSIOLRCHDHSVMVYKPPADSCKEIFSL 240
Db 181 ggelepesioalsrkpaksowvrrkd/sikvsiolrchdhsvmvykppadsckeifsl 240
0Y 241 PHMAAMSTYMRKGIITFKKAVSYFRDILAEIOLSLKKAALDQLRFNRYFNAETOTWE 300
Db 241 phmaamstymrkgiitfkkavsyfrdilaeiolslkkaaldqlrfnryfnaetotwe 300
0Y 301 CONRSYCELDIADGCHQOILLHEMLKFNHMLKKLOLHEFEYVLMQALSLFSPDRGVLOHK 360
Db 301 conrsycedldiadcqoillhemlkfnhmlkklolhefeyvlmqalslfspdrgvlohk 360
0Y 361 cgrhsycedldiadcqqlldemlklthmllkldqheeevylmqalslspdrgvqlhrt 400
Db 361 cgrhsycedldiadcqqlldemlklthmllkldqheeevylmqalslspdrgvqlhrt 400
0Y 401 ATPLMODEFGTIGS 414 -----F 400
Db 401 atplmodefgtigs 414 -----F 400
0Y 421 atplmodefgtigs 414 -----F 400
Db 421 atplmodefgtigs 414 -----F 400

```

RESULTS

AAV21799 standard; Protein; 434 AA

AC: AAY21799

14-SEP-1999 (first entry)

DE Human steroid and xenobiotic receptor (SXR)

KW Nuclear receptor; SXR, steroid and xenobiotic receptor; RXR, human;

phytoestrogen

polycystic ovary

(5) *Homo sapiens*.

FH Key

ET
ET

XX

~~XXXX~~

XXXXXX

XX
XX

XX
XX
DT

XX
XX
1666-1667

10R N-(2S)H; AAX85

New steroid and xenobiotic receptor, used to identify modulators for controlling metabolism of steroids and xenobiotics, e.g., reducing their toxicity

Claim 4; Fig 1A; 83pp; English.

The invention relates to a novel nuclear receptor polypeptide, designated SXR (steroid and xenobiotic receptor). SXR (i) forms a heterodimer with retinoid x receptor (RXR), (ii) binds to a direct or inverted repeat response element motif based on the half-site AGTCA, (iii) activates transcription through response elements present in steroid-inhibitable p450 genes, In response to a wide variety of natural and synthetic steroid hormones and (iv) is prominently expressed in liver and intestine. SXR regulates expression of catabolic enzymes, in response to many different steroids, and thus affects metabolism. SXR is a broad specificity, low affinity receptor for reducing excessive levels of steroids in the circulation. (Anti)agonists of SXR are used to regulate metabolism of steroids particularly phytoestrogens or calcium-channel blockers, to reduce steroid toxicity in subjects being treated with steroids, e.g. in cases of tuberculosis (treated with rifampin and related compounds), breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis (treated with Vitamin K), or to slow metabolism of therapeutic steroids. Also, modulating endogenous SXR is used to treat disease, particularly an agonist is used where endogenous steroid levels are excessive (e.g., Cushing syndrome); vitamin D and hypovitamin D in women; polycystic ovarian disease; II beta- α , 17- or 21-hydroxylase deficiency; 3 beta-hydroxysteroid dehydrogenase deficiency of breast, colorectal or prostatic cancer). While antagonists are used where endogenous steroid levels are too low Cells that express SXR are used to identify compounds likely to be involved in undesirable drug interactions. Antibodies specific for SXR are used in immunohistochemical testing for studying distribution/expression density of SXR, also for diagnosis and therapeutically as antagonist The present sequence represents SXR polypeptide.


```

XX His-phenanthrene X receptor (PXR) sequence.
DE
XX
XX Human: nuclear receptor; phenanthrene X receptor; PXR; CYP; CYP3A4;
KM cytochrome P-450 mono-oxygenase; drug interaction; hPXR.
XX
XX
XX Syntetec.
OS
XX Homo sapiens.
XX
XX W09948915-A1
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99MO-US08737
XX
XX 27-MAR-1998; 98DS-0079593.
XX
XX (GLAXO) GLAXO GR00P LTD.
XX
XX Kiewit SA, Willson TM.
XX
XX WPI: 1999-601202/51.
XX
XX
XX New human phenanthrene X receptor, used to identify specific modulators and
PT agents that induce expression of cytochrome P-450 mono-oxygenase -
XX
XX Example 6; Page 37; 69pp; English.
XX
XX The invention provides an isolated human nuclear receptor (designated
CC phenanthrene X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase
CC (CYP) promoter. The hPXR is used to identify its specific modulators,
CC and compounds that induce CYP3A4 expression (i.e. to identify drug
CC interactions, since CYP3A4 is involved in many biotransformations of
CC drugs). The modulators are potentially useful for associating particular
CC diseases and conditions with PXR and for treating such conditions.
CC Antibodies raised against hPXR can be used for determination and
CC purification of hPXR. The present sequence represents a histidine-6
CC tagged partial PXR (His-PXR) sequence.
XX
XX
XX Sequence 416 AA:
XX
XX
XX Query Match 66.9%; Score 1463; DB 20; Length 316;
XX Best Local Similarity 93.4%; Pred. No. 4e-137;
XX Matches 285; Conservative 0; Mismatches 0; Indels 20; Gaps 1;
XX
XX 130 SEKTGTPPLVQDLEFGQMMRELMDAQMKTFTDTFSHKRRLPGVLSQCELPESIQ 189
XX
XX 12 SEKTGTPPLVQDLEFGQMMRELMDAQMKTFTDTFSHKRRLPGVLSQCELPESIQ 71
XX
XX 190 AFSREFAAASVYKQICSLKYSLSQIKQEGSVWYKPPASQCKTFPSLTHMAMSTY 249
XX
XX 72 AFSREFAAASVYKQICSLKYSLSQIKQEGSVWYKPPASQCKTFPSLTHMAMSTY 131
XX
XX 250 MKGGISSEKAVSYERKPIPIHQISLKGAEFLQRLNFTFNATGFWGGRISYCLE 309
XX
XX 132 MKGGISSEKAVSYERKPIPIHQISLKGAEFLQRLNFTFNATGFWGGRISYCLE 191
XX
XX 310 DIAGGQVLLLEPMLEKFMKIKKIUHEEYVLMASLSPDRPVLGHRVDOIQDF 369
XX
XX 192 DIAGGQVLLLEPMLEKFMKIKKIUHEEYVLMASLSPDRPVLGHRVDOIQDF 251
XX
XX 370 AATLKSYIEFNRPQAHRLFLKIMAMLE-----FATPIQDEL 409
XX
XX 252 AATLKSYIEFNRPQAHRLFLKIMAMLE-----FATPIQDEL 111
XX
XX 410 GIGGS 414
XX
XX 312 GIGGS 316
XX
XX
XX RESULT 14
XX AAR98521

```

```

10 AAR98521 standard; Protein: 386 AA.
XX
XX AAR98521;
AC
XX 14-NOV-1996 (first entry)
XX
XX Xenopus orphan receptor 6.
DE
XX
XX Xenopus orphan receptor 6; XOR 6; steroid receptor; vitamin D;
KM hydroxybenzoate; methylbenzoate; antihydroxy.
XX
XX Xenopus laevis.
OS
XX
XX Key Location/Qualifiers
XX Domain 77..102
XX Domain 183..386
XX Domain /Label=ligand_binding_domain
XX
XX W09622390-A1.
XX
XX 25-JUL-1996.
XX
XX 16-JAN-1996; 96MO-US00058.
XX
XX 17-JAN-1995; 95DS-0374445.
XX
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX
XX Blumberg B, Evans KM, Umerson K;
XX
XX WPI: 1996-354546/35.
XX
XX N-PSDB; AAT36499.
XX
XX DNA encoding receptor polypeptide responsive to hydroxy, mercapto or
PT amino benzoate(s) - useful to regulate gene transcription
XX
XX Claim 4; Page 27-28; 42pp; English.
XX
XX
XX Xenopus orphan receptor 6 (XOR-6) (AAR98521) is a new member of the
CC steroid receptor superfamily, characterized as being responsive to
CC the presence of hydroxy, mercapto or amino benzoate(s) and as
CC regulating the transcription of associated gene(s). It shows 74%
CC identity in the DNA binding domain, and 42% identity in the ligand
CC binding domain, to the human vitamin D receptor. Recombinant XOR 6
CC can be expressed in animal cells; a cDNA clone (AAT36499) coding for
CC XOR-6 has been isolated. The recombinant XOR-6 may be used to
CC regulate gene transcription or to raise antibodies of diagnostic
CC or therapeutic appln.
XX
XX
XX Sequence 386 AA:
XX
XX
XX Query Match 41.6%; Score 910.5; DB 17; Length 386;
XX Best Local Similarity 46.2%; Pred. No. 5.1e-82;
XX Matches 192; Conservative 55; Mismatches 100; Indels 69; Gaps 10;
XX
XX 18 EDPESVSKSYNADEFGVQITFVSGIKATGVHNYMTCKGKGFRRKAKKRNARIC 77
XX
XX 14 EECVCLASNSQVQVEDADDPKIVACQDIDATYHMLTCEGCKGKTRVCKNLLISC 74
XX
XX 78 PFKKACELIKTRKQVQACRLKQESGKKKKMMMSHFAVERKALIKK-KSFRTIQ 146
XX
XX 74 PFKKACELIKTRKQVQACRLKQESGKKKKMMMSHFAVERKALIKK-KSFRTIQ 132
XX
XX 137 PLGVGGLTFEQGMMRELMDAQMKTFTDTFSHKRRLPGVLSQCELPESIQ 196
XX
XX 133 PLGVGGLTFEQGMMRELMDAQMKTFTDTFSHKRRLPGVLSQCELPESIQ 171
XX
XX 197 AKWSVVRKMLCSLKYSLSQIKQEGSVWYKPPASQCKTFPSLTHMAMSTYKKTIS 256
XX
XX 172 AKWSVVRKMLCSLKYSLSQIKQEGSVWYKPPASQCKTFPSLTHMAMSTYKKTIS 207

```


1	922.5	42.2	386	2	S4197	thyroid hormone re
2	922.5	42.2	388	3	JC710	benzoate x receptor
3	771	35.3	420	2	JC7225	vitamin D receptor
4	768.5	35.1	448	2	150451	vitamin D receptor
5	762	34.8	431	2	A41761	1,25-dihydroxyvita
6	753.5	34.5	422	2	PC4019	vitamin D receptor
7	750	44.3	427	2	A28200	vitamin D receptor
8	750	44.3	427	2	S24174	vitamin D receptor
9	748.5	34.2	425	2	JC7230	vitamin D receptor
10	731	33.4	368	2	A56197	nuclear hormone re
11	472	21.6	461	2	JC4014	steroid hormone nu
12	463	21.2	446	2	149021	retinoid x receptor
13	461.5	21.1	445	2	A56043	steroid hormone re
14	461	21.1	446	2	159454	orphan nuclear re
15	456.5	20.9	447	2	138975	nuclear orphan rec
16	426	19.5	369	2	TWCHT8	thyroid hormone re
17	426	19.5	369	2	S58211	beta-thyroid hormo
18	425	19.4	373	2	151165	gene c-erbA-beta p
19	424	19.4	373	2	C36067	thyroid hormone re
20	423	19.3	456	1	TVH08	thyroid hormone re
21	419	19.2	373	2	D36067	thyroid hormone re
22	417	19.1	461	2	A40377	thyroid hormone re
23	417	19.1	461	2	A31820	thyroid hormone re
24	417	19.1	475	2	A57035	thyroid hormone re
25	413.5	18.9	878	2	A54590	ecdysone receptor
26	411.5	18.8	536	2	A56590	steroid hormone re
27	411	18.8	464	2	A56918	retinoid x-activata
28	406.5	18.6	449	2	149018	thyroid hormone re
29	406	18.6	416	2	151096	thyroid hormone re

30	401.5	18.4	408	1	TCVCHV	thyroid hormone re
31	364	18.0	410	2	AAU917	thyroid hormone re
32	364	18.0	410	2	SI4416	thyroid hormone re
33	394	18.0	464	2	A56558	retinoic acid rece
34	393	18.0	448	2	AA4786	retinoic acid rece
35	390	17.8	410	2	S09178	thyroid hormone re
36	389.5	17.8	614	2	AA2608	thyroid hormone re
37	489	17.8	410	1	QMRSA1	thyroid hormone re
38	487	17.8	418	1	TVX1TA	thyroid hormone re
39	387	17.7	448	2	S02827	retinoic acid rece
40	387	17.7	459	2	AA1977	retinoic acid rece
41	386	17.6	444	2	151256	retinoic acid rece
42	386	17.6	448	2	S05051	retinoic acid rece
43	484	17.6	455	2	SI4512	retinoic acid rece
44	382.5	17.5	452	2	S78481	retinoic acid rece
45	382	17.5	410	2	S06410	thyroid hormone re

AL.1 (JNMF:NTS)

RESULT

thyroid hormone receptor homolog - African clawed frog

Q: Date: 20-May-1994 #sequence_revision 26 May-1995 #text_change 20-Sep-1995

R. Smith, D.P.; Mason, C.S.; Jones, E.A.; Old, K.W.

ATTILIO: A novel nuclear receptor

A:Accession: S41497

A: molecule type: mRNA

A;CROSS-REFERENCES: EMBL:X75163; NID:q410517; PIDD:CAA53006.1; PIDD:q410518

C;Keywords: zinc finger

Query Match: 42.28; Score 922.5; IH 2; Length 386;

Matches 194; Conservative 54; Mismatches 99; Indels 69; Gaps 10.

18 EDTFVPGKPSVNADEEVGGPQICRVGDKATGYHFNMTGEGCKCFRRAMKRNARLK 77

DB 14 FFEDASNSCG1GHEDIDGDPKICRA:GDKRATGYHFNAMICFJOKCFPRRAVKRNI,RLS* 73

78 PERKACHETKI PROCAKRIKOTIESOMKININSHAVERRAIKKK-KSHICTO 1 *

74 PF-QNSCVINKSNRHCQACRLKKCLDTCMKKFLMSIAAVFQKRALIKKRIKLIKLEPPT 14

137 PLOVOGLITEOKMMIKH.MDAOMKTEPTTSHKXNH.I.VI.SSOTEL.P.SLOAI.SHEA 19

133 PPGA-SI,TPGOUHFI,TOI,VC,AHT(KT,FI)FN,T,HSKNR.....PIK... 17

QY 197 AKWSQVRKDJLSLKVSLQJRGELKGSVWNYKPPAJSGGKFTFSLPHMAJMYMKJ125 29

172 - - - - - KSSDPT - - QEPQAT5 - - SEAF1.MLPHISDLVTYMIKG115 20

QY 257 FAKVISYFRDLP I HDQISLJ.KGAFFI.CQJ.KFNTV'NAH.TGTWECGRJ.SYCI.EDT-AGGF 31

DB 208 FAKMLPYFKSLDIEDQIALKGSVAEVSIRFNTVFNSITNTWECGPFTYDTEDMFIAGF 26

QY 316 QQLJ,EPMLKHYMLKKIQJ,HEHYVI,MOAISI,FSPIRPIVLQHRVLOJ,OFPAIILXS 37

Db 268 KÖLFLEPLVRIRHRMRKI,NI,ÜSEFYAMMAI,SI'ASDRPGVCJWEK İÖKI,ÜFHIAL,IT,XI) 32

376 YIECNR-PÖPAHRELFKIMAMLETFE-----ATPLMÖELFES 410

Db 328 F1DSÖRPPSPÖNRILYPRIMECT.TELKIVNDHSKÖL.F1WD1ÜPLAIP1.MKRVF3 483


```

QY 191 PSREFAKMSQYKRDLSLKV-----LQKGEQSVNKKPPADSGKEIFSLPHMAM 246
DB 179 LSHASDSHSPRESV-DIKVNPNNILMYQFGS-----SPISSEEGSGSFMLPLADI 233
QY 217 SYFMKGIISFAKVISYFHDLPIDQISLKGAFELCOLRNTVNAFTGWECCR--L 304
DB 234 VASVIOKVIQFAKMLPGFRELTAEDQIALKSSALFVIMLRNOSFNLEDMWSGAPDF 293
QY 305 SCGLDP-TAGGFOQALLERMLKFKHMLKKLQJHEHYVIMQALSLSPDRGVLOHRYVD 363
DB 294 KQVISIVIKAGHTLELEPLKPVQVOKKLNQJFEHVMMLACILSPDRGVQDHARLE 353
QY 364 QJQJPAIILKSVIEGNNRQVPAHRELEKIMATLTF----- 400
DB 354 ALQDRISTELQVYOLH--HPGRKILYAKMIQKLAULKSLNEHSKQYRSLSPREHSMQ 411
QY 401 APLMOELPG 410
DB 412 LTPLELVSG 421

RESULT 10
A56197
nuclear hormone receptor MB67 - human
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 20-Sep-1999
C:Accession: A56197
R:Baes, M.; Gullik, T.; Choi, H.S.; Martinoli, M.G.; Simha, D.; Moore, D.D.
Mol. Cell. Biol. 14, 1544-1552, 1994
A>Title: A new orphan member of the nuclear hormone receptor superfamily that interacts
A:Reference number: A56197; M01D:94158627
A:Accession: A56197
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BAE>
A:Cross-references: GB:210425; GB:129263; NID:9458541; PIDN:CAAB3016.1; PID:9458542
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: Zinc finger
F:9-270/domain: erba transforming protein homology <ERBA>

Query Match 33.4%; Score 731; DB 2; Length 348;
Best local similarity 40.5%; Pred. No. 6, le-50;
Matches 157; Conservative 59; Mismatches 100; Indels 72; Gaps 6;

QY 41 CRVGDRAKGYHNVNTGCKGKFFRRAMKRNALRCGPERGACETTRKRCQACRLR 100
DB 11 CVVCGQATGYNNATCGCKGKFFRRVSKSIGTPGPF-AGSGEVSKTQRHHCACRLQ 69
QY 101 KTLSSMKKEMTNSDEAVERRALLKRKKSERTGTQPLAVGSLTHQRMMIRELMDQMK 160
DB 70 KCLDAMRKMKMLSAFALAKRAKQVORRAQOTPVQ---LSKQDEPLFKLILGAHTR 123
QY 161 TDTLTHSHKKNFRLGVSSNGELPESTLQAPREFAKMSQYKRDLSLKVSLQJRGEGS 220
DB 124 HMTIMEQVQRPRAHCTIHQ-PLPTTAP----- 153
QY 221 SWNNKPPADSGKEIFSLPHMAMSLYFPGIISFAKVISYFHDLPIDQISLKGAA 280
DB 154 -----VPLVTHRADINITWVIGVIKFTKDLVFRSLPDEQISLKGAA 198
QY 281 PHLQJLRNTVNAETSTGEVQGLSYGLEDTAG-GTQVLLERMLKFNHMLKKLQJHEE 339
DB 199 VETGIVLNTTQCLQNTLQGLRYTLHDGARVQVQVPELLELFHFHGTLPKRLQJQPE 258
QY 340 YVIMQALSLSPDRGVLOHRYVDLQJQDFALITKSVIEGNNRQVPAHRELEKIMATL 399
DB 259 YVIMQALSLSPDRGVLOHRYVDLQJQDFALITKSVIEGNNRQVPAHRELEKIMATL 318
QY 400 PAT -----PLMOET 408
DB 319 IRLSINAVGYOLHIGGLSMMMLTQET 346

```

```

RESULT 11
JC4014
steroid hormone-nuclear receptor NER - human
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
C:Accession: JC4014
R:Shinar, D.M.; Endo, N.; Rutledge, S.J.; Vogel, R.; Kodan, G.A.; Schmidt, A.
Gene 147, 273-276, 1994
A>Title: NER, a new member of the gene family encoding the human steroid hormone nucl
A:Reference number: JC4014; M01D:95011628
A:Accession: JC4014
A:Molecule type: mRNA
A:Residues: 1-461 <SH>
A:Cross-references: GB:007132; NID:9641961; PIDN:AAA61783.1; PID:9641962
A:Experimental source: osteosarcoma cells SVOS-2/R10
C:Genetics:
A:Gene: GDB:UNR
A:Cross-references: GDB:149570; OMIM:600480
A:Map position: 19q13.4-19q13.3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: steroid hormone receptor
F:85-381/domain: erba transforming protein homology <ERBA>
F:87-154/domain: DNA binding #status predicted <HN>

Query Match 21.6%; Score 472; DB 2; Length 461;
Best local similarity 28.3%; Pred. No. 1, 9e-29;
Matches 122; Conservative 80; Mismatches 119; Indels 110; Gaps 14;

QY 37 GQUTRVYQDRAITGHEVNTGCKGKFFRRAMKRNALRCGPERGACETTRKRCQ 95
DB 83 GHELCRVGQVQKASQPHVNTLSCGCKGKFFRRVYAGAKRYAKGQGTQMDAPMKRQV 142
QY 96 ACRLKCTCSGKKKEMISDEAVERRALLKRKKSERTGTQ-PLAVQV----- 142
DB 143 QCLRLKCKEAGMKRECVLSDEIRKK--IKQVQVEQSQSQSVGVQSSSSASGIGA 200
QY 143 -----LTHQRMMIRELMDQMKLTDTLTHSHKKNFRLGVSSNGE 183
DB 201 SFGSGAGSNGSGEGEGVLTAAQELMIOI VAAQIQNKRSFS----- 244
QY 164 LPESIQASREFAKMSQYKRDLSLKVSLQJRGEGSVNKKPPADSGKEIFSLPHM 243
DB 245 -----DQKVTYWP-----LQAD-----PQSRAPQVFA--HF 271
QY 244 ADMSTYMKGIISFAKVISYFHDLPIDQISLKGAFELCOLRNTVNAFTGWECCR-- 301
DB 272 TELALISVQELVDPAKQVPGFQJQGRDQIALKASTELIMLETARKYNET---ECIT 328
QY 302 --GRUSYCIHD-TAGGFOQALLERMLKFNHMLKKLQJHEHYVIMQALSLSPDRGVLO 358
DB 329 ELKQDTYSKDDPHRAGLQVEFINLPERSRAMKRLGIDDAVYALLAINISADHPNVQ 388
QY 355 HRVAVQJQDFALITKSVIEGNNRQVPAHRELEKIMATL-----EPA----- 401
DB 389 PGVPAQQLQVFEALISYTRIKRQVQILPFRPMKILVSTKLTSSVSHQVFAQLQJRK 448
QY 402 -TPLMOELPG 411
DB 449 LPLLSLEIMDV 459

RESULT 12
149021
retinoid X receptor interacting protein No.15 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: 149021
R:Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-85, 1995
A>Title: Isolation of proteins that interact specifically with the retinoid X recepto
A:Reference number: A57664; M01D:95280959

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2002, 02:37:30 ; Search time 21.95 Seconds

(without alignments)
633.789 Million cell updates/sec

Title: US-09-276-935b-14

perfect score: 2187

Sequence: 1 LEVREKESNNMADPVEHCET.....AMLEPAPIMQELFCITGS 414

Scoring table: H40SUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Testing first 45 summaries

Database: Swissprot_39*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2165	99.0	434	1	PKR_HUMAN
2	1675.5	76.6	431	1	PKR_MOUSE
3	1656.5	75.7	431	1	PKR_RAT
4	774	35.4	422	1	VDR_XENLA
5	768.5	35.1	448	1	VDR_GOTJA
6	768	35.1	451	1	VDR_CHICK
7	762	34.8	423	1	VDR_RAT
8	751.5	34.5	422	1	VDR_MOUSE
9	750	34.3	424	1	VDR_BOVIN
10	750	34.3	427	1	VDR_HUMAN
11	731	33.4	348	1	NR13_HUMAN
12	685.5	31.3	358	1	NR13_RAT
13	680	31.1	358	1	NR13_MOUSE
14	472	21.6	461	1	NRH2_HUMAN
15	469.5	21.5	445	1	NRH3_MOUSE
16	463	21.2	446	1	NRH2_MOUSE
17	461.5	21.1	445	1	NRH3_RAT
18	461	21.1	447	1	NRH2_RAT
19	456.5	20.9	446	1	NRH3_HUMAN
20	433	19.8	386	1	THB_BRARE
21	431.5	19.7	395	1	THB_PAROL
22	428.5	19.6	757	1	ETR_LOCTO
23	426	19.5	369	1	THB_CHICK
24	426	19.5	461	1	THB_HUMAN
25	425	19.4	373	1	THB_RANCA
26	424	19.4	373	1	THBA_XENLA
27	423.5	19.4	675	1	ECR_AEDAE
28	423	19.3	416	1	THA_HIPPI
29	423	19.3	476	1	THB2_HUMAN
30	419	19.2	414	1	THBB_XENLA
31	417	19.1	411	1	THB1_SHEEP
32	417	19.1	461	1	THB1_MOUSE
33	417	19.1	475	1	THB2_MOUSE

34	413.5	18.9	878	1	PKR_DROME	P44821 drosophila
35	413	18.9	461	1	THB1_RAT	P18114 ratius nov
36	413	18.9	514	1	THB2_RAT	P37826 ratius nov
37	411.5	18.8	427	1	THA_BRARE	O98867 brachydanio
38	411.5	18.8	536	1	ECR_CHILE	P49882 charomimus
39	406	18.6	416	1	THA_PAROL	O91241 paratichthy
40	402.5	18.4	556	1	ECR_MOUSE	P49883 mus musc
41	401.5	18.4	408	1	THA_CHICK	P04625 gallus gall
42	397.5	18.2	402	1	THA_APTPA	O42295 aptenodytes
43	397.5	18.2	402	1	THA_PYGAD	O42450 pygostolus
44	395.5	18.1	401	1	THA_CAIMO	O90482 caillina mus
45	394	18.0	410	1	THA1_SHEEP	O28570 ovis aries

ALIGNMENTS

RESULT 1
PKR_HUMAN STANDARD: PRT: 434 AA.
ID PKR_HUMAN
AC O75469
DT 15-JUL-1999 (Ref. 38, Created)
DT 15-JUL-1999 (Ref. 38, Last sequence update)
DT 20-AUG-2001 (Ref. 40, Last annotation update)
DE ORPHAN NUCLEAR RECEPTOR PKR (PREGNANE X RECEPTOR) (ORPHAN NUCLEAR RECEPTOR PART).
GN NR12 OR PKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NRI1;Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Liver;
RX MEDLINE=98395174; PubMed=9727070;
RA Lehmann J.M., McKee D.D., Watson M.A., Willson T.M., Moore J.T., Klierer S.A.;
RT "The human orphan nuclear receptor PKR is activated by compounds that regulates cypl3A4 gene expression and cause drug interactions";
RL J. Clin. Invest. 102:1016-1023(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE: Liver;
RX MEDLINE=98445350; PubMed=9770465;
RA Bettlison G., Heidrich J., Svensson K., Asman M., Jendeborg L., Sydow-Hackman M., Ohlsson R., Postlund H., Blomquist P., Berkenstam A.;
RT "Identification of a human nuclear receptor PKR as a new signaling pathway for cypl3A induction";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12208-12211(1998).
RN [3]
RP PREGNANE: ORPHAN RECEPTOR: ITS NATURAL LIGAND IS PROBABLY PREGNANE, BINDS TO A RESPONSE ELEMENT IN THE CY3A4 GENE PROMOTER.
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, COLON, AND SMALL INTESTINE.
CC -1- INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH AS PREGNENOLONE AND PROGESTERONE.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
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CC EMBL: AF061056; AAC05436.1; .
CC EMBL: AF084645; AAC64558.1; .
CC MIM: 603065; .
CC InterPro: IPR000536; Hormone_rec_114.


```

DB 240 LADVSTWFKGVINFAKVISYFRDLPLEDOJSLKGAFFEMCLIFNTMDPIETQWEG 299
QY 403 RLSTCLFEPAGGFCOLLLEPMKLFHYMKKLUHEEYVLMQALISFSPDRPVUQHRV 362
DB 400 RLAVFEPENSGFOLLLDPLMKFHCMLKLQLEEEYVLMQALISFSPDRPVUQHRV 359
QY 363 DOJOFALITKSYJECNRPOFAHREPLFKIMAMTE:-----FAI 402
DB 360 DOJOFKALITKAVITENSRPYAHREPLFKIMAVITELKSNAGUOVLKLUQSHRPAT 419
QY 403 PLMOELFGIT 412
DB 420 PLMOELFST 429

RESULT 3
PKR_RAT STANDARD: PRT: 431 AA.
AC Q9RIAT:
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ORPHAN NUCLEAR RECEPTOR PKR (PREGNANE X RECEPTOR).
GN NR112 OR PKR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX M._taxid-10116;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN SPRAGUE-DAWLEY;
MEDLINE-99345883; PubMed-10415106;
KA Zhang H., Lechlyse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;
RT "Rat pregnane X receptor: molecular cloning, tissue distribution, and
RT xenobiotic regulation."
RL Arch. Biochem. Biophys. 368:14-22(1999).
CC -1- FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY
CC PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER (BY
CC SIMILARITY).
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DB EMBL: AF161377; A047214.1;
DB InterPro: IPR000536; Hormone_rec_119.
DB InterPro: IPR001723; Steroidhormone_receptor.
DB InterPro: IPR001628; Z1-C4.
DB Pfam: PF00104; hormone_rec_1.
DB Pfam: PF00105; Z1-C4.1.
DB PRINTS: PR00047; STEROIDRECEP.
DB PRINTS: PR00350; VITAMINDR.
DB PRINTS: PR00498; STEROIDRECEP.
DB SMART: SM00430; H011.1.
DB SMART: SM00399; ZNF_C4.1.
DB PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KM Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KM Zinc-finger.
FT DNA_BIND 38 104 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 38 58 C4-TYPE.
FT ZN_FING 74 99 C4-TYPE.
FT DOMAIN 105 201 HINGE.
FT DOMAIN 202 431 LIGAND-BINDING.
SEQUENCE 431 AA; 49660 MW; 48545F21F9459697 CAC64;

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Query Match 75.7%; Score 1656.5; DB 1; Length 431;
Best Local Similarity 72.8%; Pred. No. 170-126;
Matches 313; Conservative 41; Mismatches 55; Indels 21; Gaps 2;

QY 3 VKPESWNAHDFVGEETESVPCQSYNADEWGGDQICWCGKALGYHFNWATCEGK 62
DB 1 MRPEPKNNHVLGVREHADVLEPP-INVDEKGLDQICWCGKALGYHFNWATCEGK 59
QY 63 GEFRRAMKNAKLKTPRKACLETETKTRQVQACNLKLTLSQMKKEMTSDPAVEER 122
DB 60 GEFRRAMKNNVLRGPERKGTCTETKTRKQVQACNLKLTLSQMKKEMTSDPAVEER 119
QY 123 ALIKRKRKRTQPIGVQCITEFGKRMKELMAGCKTPTDTSHEKNNRLHVSLSG 162
DB 120 ALIKRKRKRETEAPPFGQDTEEOALDQELMAGQITPTDTSHEKNNRLHVSLSG 179
QY 183 ELPESTQAPSHFEAKNSQVNRKDLSTKNSLQIKGHEWNSWNRKPMASAKETSLD 242
DB 180 ELPEVQASLELPATQSJMKNSVIMKISVOLRGELSTIMNVQPSKSGKELPLD 239
QY 243 MADNSTWFKGISFAKVISYFRDLPLEDOJSLKGAFFELCOLRENTVMAETGWEG 402
DB 240 LADVSTWFKGVINFAKVISYFRDLPLEDOJSLKGAFFEMCLIFNTMDPIETQWEG 299
QY 403 RLSTCLFEPAGGFCOLLLEPMKLFHYMKKLUHEEYVLMQALISFSPDRPVUQHRV 402
DB 400 RLAVFEPENSGFOLLLDPLMKFHCMLKLQLEEEYVLMQALISFSPDRPVUQHRV 359
QY 363 DOJOFALITKSYJECNRPOFAHREPLFKIMAMTE:-----FAI 402
DB 360 DOJOFKALITKAVITENSRPYAHREPLFKIMAVITELKSNAGUOVLKLUQSHRPAT 419
QY 403 PLMOELFGIT 412
DB 420 PLMOELFST 429

RESULT 4
VDR_XENLA STANDARD: PRT: 422 AA.
AC 013124;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN VDR OR NR111.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloide; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID-8355;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-97407674; PubMed-9165021;
KA Li Y.C., Betawitz G., Jueppner H., Denney M.B.;
RT "Cloning and characterization of the vitamin D receptor from Xenopus
RT laevis."
RL Endocrinology 118:2447-2453(1997).
CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
CC LEVEL IN SMALL INTESTINE AND SKIN.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 57.61 THEN DECREASES TO THE LEVEL
CC SEEN IN ADULT.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC

```

001. *Archosauroidae*; *Aves*; *Neornithidae*; *Calliformes*; *Phasianidae*; *Phasianinae*;

QY 239 11P1MA1M51YMPK01SPAKVISYR0LPI1HQ1SLK0AAPEH0Q0LKFNVPVNAFT0T 298

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Db      1  MIPHLADVSVJQKIVGEAKMKIPQFDLTAEQDIALICKSSAPVIMKSNOSTMEIENS 306
      2  299  WECC--LSTYLED-IAAGFQULLEPMLAKHYMKLQULHEEYVIMQASISLSPORRG 355
      3  307  WTGSGNDFKRYKVSIVTVAGHSMQLEPLVKKYQVGLKINLHFEFVILMAICILSPDRG 366
      4  356  VUQHVVYUOLQFOVALTKSYLFPNNRQPAHRLPLKIMAMTLER----- 400
      5  367  VQDTLSVESTQDKISDTLTQYTRCHRPSPGSRLLYAKMKQLADIKLSNEHSKYQCLIS 426
      6  401  -----APPLMQLFPG 410
      7  427  FQFHSMLPLVLEVRG 444
      8
      9  RESULT 6
     10  VDR_CHICK STANDARD: PRT: 451 AA.
     11  0A2392;
     12  15-DEC-1998 (Rel. 37, Created)
     13  15-DEC-1998 (Rel. 37, Last sequence update)
     14  15-JUN-1999 (Rel. 38, Last annotation update)
     15  VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
     16  VDR OR NR11.
     17  Gallus gallus (Chicken).
     18  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     19  Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;
     20  Gallus.
     21  NCBI_TaxID=9011;
     22  [1]
     23  SEQUENCE FROM N.A.
     24  STRAIN LECHON; TISSUE: Kidney;
     25  MEDLINE-9723369; PubMed-9056239;
     26  Lu Z., Hanson K., Deluca H.F.;
     27  "Cloning and origin of the two forms of chicken vitamin D receptor.";
     28  Arch. Biochem. Biophys. 349:99-106(1997).
     29  [2]
     30  SEQUENCE OF 45-114 FROM N.A.
     31  MEDLINE-87149040; PubMed-3029866;
     32  McDowell D.P., Mandelstorf D.L., Pike J.W., Hausler M.R.,
     33  O'Malley B.W.;
     34  "Molecular cloning of complementary DNA encoding the avian receptor
     35  for vitamin D.";
     36  Science 255:1214-1217(1987).
     37  RL
     38  -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
     39  THE EXPRESSION OF HORMONE SENSITIVE GENES.
     40  CC
     41  -1- SUBCELLULAR LOCATION: NUCLEAR.
     42  CC
     43  -1- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE OF
     44  ALTERNATIVE INITIATION CODONS.
     45  CC
     46  -1- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.
     47  CC
     48  -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
     49  A DNA-BINDING DOMAIN AND A C-TERMINAL STROOPID-BINDING DOMAIN.
     50  CC
     51  -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
     52  NR1 SUBFAMILY.
     53  -----
     54  CC
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     56  between the Swiss Institute of Bioinformatics and the EMBL outstation.
     57  CC
     58  The European Bioinformatics Institute. There are no restrictions on its
     59  use by non-profit institutions as long as its content is in no way
     60  modified and this statement is not removed. Usage by and for commercial
     61  entities requires a license agreement (see http://www.isb-sib.ch/annouce/
     62  or send an email to license@isb-sib.ch).
     63  CC
     64  EMBL: AF011356; AAB62579.1;
     65  InterPro: IPR000546; Hormone_rec_119.
     66  InterPro: IPR001626; ZF-C4.
     67  Pfam: PF00104; hormone_rec_1.
     68  Pfam: PF00105; ZF-C4.1.
     69  PRINTS: PR00047; STEROIDINER.
     70  PRINTS: PR00450; VITAMINDR.
     71  SMART: SM00450; HOLL1.1.
     72  SMART: SM00399; ZNF_C4.1.
     73

```

Query	8	SWNH	-----	ADVFHCEDTSSVPRKPSNADREKGGVIGCVVQTKAGYHFNMM	57	
Query Match				45.1%	Score 768; DB 1; Length 451;	
Best Local Similarity				38.0%;	Prod. No. 1054;	
Matches	172;	Conservative	71;	Mismatches	148; Indels 62; Gaps 10;	
DB	7	SWDQOQSMAYI	PIADMDTVAASTSLP	-DPAADIFRNV	-PRIGVGVDRATGFHFHNAV	63
QY	58	CEGCKGFPRKAKRKAKR	KCEPRKACCELTETKTRQVQACPLKCTLSGMRKEMIMSDPA	117		
DB	64	CEGCKGFPRKSKKKKAMPCEP	-MDCKITIKNRKHVQACRLKRVVDICMRKEFTLLDPE	122		
QY	118	VEERKALTRKRSKSTGTQPLGVLCTEQRMMFELMADQKTEFTTSHKNEPL	--	175		
DB	123	VORKEHMLKKRKEPALKESLKP	-LSEGGQKVIDTLLEHHKRTFDITTSQNRKRPVVR	181		
QY	176	-----	GVLSGCEGLDESIOASREFAAKWSQVKRL	SLKSLQKCHENSW	223	
DB	182	SKFSRMAVTHSSSVSQP	SPSHDSNMVGGDAAPFPEHMEQMSNLTLSEPSDPSM	241		
QY	224	NYKPADGCGKEETEL	ILHMANSTMYMKGI	ISFAKVISYEDQDPLDGLSILKNAFEL	283	
DB	242	NIELPH	-----	LPHMLADLVSTSLQKVI	GFPAKMLRFDLLAHVQIALKSSALPV	294
QY	284	QULREIVENATGTWEGRR	--	LSYGLD-LTANGFQVLLTEPMLEHMLKKLQLEHEFY	340	
DB	295	IMLRNQSTFEDMSMTGSSNIP	KYKVSIVTQAGHSMLLEFLVQVATLKLNLBHEFH	354		
QY	341	VLMQALISFSDPRGVYLOHVVQLOEQPAILTKSV	IECNRPQVAPHEPLTKIMMTPF	400		
DB	355	VILMACTISPRGPOVDTSEVSTQDRISDILLQYIK	GRHPSPGSRDLAYAKIOCLDL	414		
QY	401	-----	ATPLMGELG	410		
DB	415	RLSLEHRSKQYRCISFOPHSMQILVILEVGG	447			
RESULT	7					
VDR_RAT						
VDR_RAT		STANDARD		PKT:	423 AA.	
AC	P13053;					
DT	01-JAN-1990 (Rel. 13, Created)					
DT	01-JAN-1990 (Rel. 13, Last sequence update)					
DT	15-JUL-1999 (Rel. 48, Last annotation update)					
DE	VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).					
GN	VDR OR NR111.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxId=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE=89071726; PubMed 2849110;					
RA	Burmesler J.K., Wiese R.J., Maida N., Deluca B.;					
RT	"Structure and regulation of the rat 1,25 dihydroxyvitamin D3					
RT	receptor";					
RL	Proc. Natl. Acad. Sci. U.S.A. 85:9499-9502(1988).					
RN	[2]					
RP	SEQUENCE OF 58-423 FROM N.A.					


```

DB  B0 RLKRGVDIGMKKEPFLTEFVQRRKFMIMKKKEEDALKSLRPR LSHPOQHIALILDA 138
QY  156 QMKTEPTTFSHKRNRLP--GVLSGCTLP-----ESTQAPSRP--EAAKWS 200
DB  139 HIKTYDPTYSDFQFRPVAVNDSGSPRPTLSFGSSSSNSDLYTPSLDMEPASF 198
QY  201 QVRKLGSLKVALDQKGGGQVWYKPRPADSGKEFSLPLPMAMSTYMKGLISPAKV 260
DB  199 TM--DL-----NEEGS---DDPSVTIDLSPLSMPLHIALVSTISQKVLGFAKM 242
QY  261 ISYERDPLEDQISLTKGAPELVLQRPNTVNAETGECRLSYCEJDT---AGSPQ 317
DB  243 IGFEDHLSDDQIVLTKSSALFVIMLRNSQSTMDMSQSDYKDDITVVSAGHTL 302
QY  318 LLEPRKLFHYMLKKLQULHEEYVLMQALSLSPRPQVLOHVVQLOQDFATLKSY 377
DB  303 ELLEPLKQVGLKKKLNHEEFVILMGLVSPDRPGVAKLEVALQDKISNTLYTI 362
QY  378 FGNRPQPAHRLFLKIMAMLTFF-----ATPLMDELFG 410
DB  364 KGRHPPSHSLYAKMIQKIALDKSLNPHSKQYKSLSPQENSKLIPVLEVG 418

RESULT 9
VDR_BOVIN
ID  VDR_BOVIN          STANDARD:      PRT:      424 AA.
AC  Q28Q47.
DT  01-NOV-1997 (Rel. 45, Created)
DT  01-NOV-1997 (Rel. 45, Last sequence update)
DT  15-JUL-1999 (Rel. 48, Last annotation update)
DE  VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
CN  VDR OR NR111.
OS  Bos taurus (bovine).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxId=9913;
RN  111
RP  SEQUENCE FROM N.A.
RX  MEDLINE:97044797; PubMed:8880453;
RT  Nelbers H.L., Kosworth B.T., Reinhardt T.A.;
RL  "Nucleotide sequence of the bovine vitamin D3 receptor.";
CC  J. Dairy Sci. 79:1313-1315(1996).
CC  -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC  THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC  -1- SUBCELLULAR LOCATION: NUCLEAR.
CC  -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC  A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC  -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC  NR1 SUBFAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: 050200; AAR01543.1;
DR  HSSP: P03372; IBCO.
DR  InterPro: IPR000516; Hormone_rec_1fg.
DR  InterPro: IPR001628; z1-c4.
DR  Pfam: PF00104; hormone_rec_1.
DR  Pfam: PF00105; z1-c4; 1.
DR  PRINTS: PR00047; STROIDEFINGER.
DR  PRINTS: PR00350; VITAMINDR.
DR  SMART: SM00430; BCL1; 1.
DR  SMART: SM00399; ZNF_C4; 1.
DR  PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW  Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW  Zinc-finger; Phosphorylation.
FT  DNA_BIND 21 46
NUCLEAR RECEPTOR-TYPE.

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FT  ZN_FING 21 41 C4-TYPE.
FT  ZN_FING 57 81 C4-TYPE.
FT  DOMAIN 87 188 HINGE.
FT  DOMAIN 189 424 LIGAND-BINDING.
SQ  SEQUENCE 424 AA; 47957 MW; E9E24926CE38C87D CRC64;

Query Match 34.38; Score 750; Dh 1; Length 424;
Best Local Similarity 40.38; Pctid No. 2,76-59;
Matches 166; Conservative 62; Mismatches 146; Indels 48; Gaps 8;

QY  38 PQRGVDKATVGHVFNWTCGGCKGFFRANKRNARICPRGAGVTPKTRGQAG 97
DB  18 PRIGVGDVATVGFHFNAMTCHCKGFFRANKRKAFLTCGF NGDKRITKDNRRHQCAC 76
QY  98 RLKRCLESGMKRKMIMSDAEVERKALKRKKSERTGTQPLGVGLTEFQRMIRLMA 157
DB  77 RLKRGVDIGMKKEPFLTEFVQRRKFMIMKKKEEDALKSLRPR LSHPOQHIALILDA 138
QY  158 QMKTEPTTFSHKRNRLPGLGVSSG---GELPESIQASREFAKWSYVKRDP----- 207
DB  136 HIKTYDPTYSDFQFRPVAVNDSGSPRPTLSFGSSSSNSDLYTPSLDMEPASF 198
QY  208 ---SLKVALDQKGGGQVWYKPRPADSGKEFSLPLPMAMSTYMKGLISPAKVSYF 264
DB  194 MDSSTPSMDLSEHSD--DDPSVTIDLSPLSMPLHIALVSTISQKVLGFAKMTPGF 242
QY  265 RDEPLEDQISLTKGAPELVLQRPNTVNAETGECRLSYCEJDT---AGSPQ 317
DB  249 KDLSEHDSQIVLTKSSALFVIMLRNSQSTMDMSQSDYKDDITVVSAGHTL 302
QY  322 PMKTFHYMLKKLQULHEEYVLMQALSLSPRPQVLOHVVQLOQDFATLKSY 377
DB  309 FLKQVGLKKKLNHEEFVILMGLVSPDRPGVAKLEVALQDKISNTLYTI 362
QY  382 PQPAHRLFLKIMAMLTFF-----ATPLMDELFG 410
DB  369 PPGSHSLYAKMIQKIALDKSLNPHSKQYKSLSPQENSKLIPVLEVG 420

RESULT 10
VDR_HUMAN
ID  VDR_HUMAN          STANDARD:      PRT:      427 AA.
AC  P11473.
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
CN  VDR OR NR111.
OS  Homo sapiens (human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX  NCBI_TaxId=9606;
RN  111
RP  SEQUENCE FROM N.A.
RX  MEDLINE:88217867; PubMed:2835767;
RT  Baker A.R., McDonnell D.P., Hughes M., Tisip T.M., Manolagiotis D.J.,
RT  Haussinger M.K., Pike J.W., Shine J., O'Malley B.W.;
RT  "Cloning and expression of full-length cDNA encoding human vitamin D
RT  receptor.";
CC  Proc. Natl. Acad. Sci. U.S.A. 85:3294-3298(1988).
RN  121
RP  SEQUENCE FROM N.A.
RX  MEDLINE:92379084; PubMed:1324736;
RT  Goto H., Chen K.S., Prall J.M., Deluca H.F.;
RT  "A single receptor identical with that from intestine/1473; cells
RT  mediates the action of 1,25-dihydroxyvitamin D-3 in B6 cells.";
RT  Biochim. Biophys. Acta 1132:103-108(1992).
RN  131
RP  SEQUENCE FROM N.A.
RX  TISSUE-Lens epithelium;
KW  Rae J.L., Shepard A.R.;
RT  Submitted (Sep-1997) to the EMBL/GenBank/DBJ databases.

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RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 97455842; PubMed 9212063;
 RA Miyamoto K., Kesterson R.A., Yamamoto H., Taketani Y., Nishiwaki E.,
 RA Miyamoto S., Hume Y., Morita K., Takeda E., Pike J.W.;
 RT "Genital organization of the human vitamin D receptor chromosomal
 RT gene and its promoter."
 RL Mol. Endocrinol. 11:1165-1179(1997).
 RN [15]
 RP SEQUENCE OF 24-90 FROM N.A.
 RX TISSUE: foetal blood;
 RX MEDLINE 9410242; PubMed 1450412;
 RA Yu X.-F., Medsall H., Hestinger F.G., Manolagas S.C.;
 RT "Vitamin D receptor expression in human lymphocytes: Stipat
 RT reagents and characterization by western blots and DNA
 RT sequencing."
 RL J. Biol. Chem. 266:7588-7593(1991).
 RN [16]
 RP VAPJANIS 310 45 AND 310 74;
 RX MEDLINE 89012761; PubMed 2849209;
 RA Hughes M.R., Malloy P.J., Kleeback D.G., Kesterson R.A., Pike J.W.;
 RA Feldman D.; of Malloy P.W.;
 RT "Point mutations in the human vitamin D receptor gene associated with
 RT hypocalcaemic rickets."
 RL Science 242:1702-1705(1988).
 RN [17]
 RP VAPJANIS 310 45;
 RX MEDLINE 9416443; PubMed 841803;
 RA Yari H., Ozono K., Miyake H., Nagashima K., Kurono Y., Pike J.W.;
 RT "A new point mutation in the deoxythymine acid-binding domain of
 RT the vitamin D receptor in a kindred with hereditary
 RT 1,25-dihydroxyvitamin D resistant rickets."
 RL J. Clin. Endocrinol. Metab. 76:509-512(1993).
 RN [18]
 RP VAPJANIS 310 50;
 RX MEDLINE 9155984; PubMed 1652804;
 RA Saito T., Ito M., Takada E., Kubodoh H., A.H.M., Naito E., Yokota I.,
 RA Sone T., Pike J.W., Kuroda Y.;
 RT "A unique mutation in the vitamin D receptor gene in three Japanese
 RT kindreds with vitamin D-dependent rickets type II: utility of single
 RT strand conformation polymorphism analysis for heterozygous carrier
 RT detection."
 RL Am. J. Hum. Genet. 49:668-674(1991).
 RN [19]
 RP VAPJANIS 310 80;
 RX MEDLINE 91125470; PubMed 2177843;
 RA Sone T., Marx S.J., Liberman U.A., Pike J.W.;
 RT "A unique point mutation in the human vitamin D receptor chromosomal
 RT gene confers hereditary resistance to 1,25-dihydroxyvitamin D."
 RL Mol. Endocrinol. 4:624-631(1990).
 RN [10]
 RP VAPJANIS 310 80;
 RX MEDLINE 94149429; PubMed 810648;
 RA Malloy P.J., Weisman Y., Feldman D.;
 RT "Hereditary 1,25-dihydroxyvitamin D resistant rickets resulting
 RT from a mutation in the vitamin D receptor deoxythymine
 RT acid binding domain."
 RL J. Clin. Endocrinol. Metab. 78:313-316(1994).
 RN [11]
 RP VAPJANIS 310 2/4;
 RX MEDLINE 94415633; PubMed 8492055;
 RA Kristjansson K., Rot A.R., Howison M., O'Riordan J.L.H., Hughes M.R.;
 RT "Two mutations in the hormone-binding domain of the vitamin D
 RT receptor cause tissue resistance to 1,25-dihydroxyvitamin D3."
 RL J. Clin. Invest. 92:12-16(1993).
 RN [12]
 RP VAPJANIS 310 45 AND 116 47;
 RX MEDLINE 95129267; PubMed 7828449;
 RA Rot A.R., Howison M., Kristjansson K., Jaisi H., Hughes M.R.;
 RA O'Riordan J.L.H.;
 RT "Two mutations causing vitamin D resistant rickets: modelling on the
 RT basis of steroid hormone receptor DNA-binding domain crystal
 RT structures."

RL J. Clin. Endocrinol. (Oct) 41:581-590(1994).
 RN [13]
 RP VAPJANIS 310 45;
 RX MEDLINE 96272879; PubMed 8675579;
 RA Liu H.-C., Malloy P.J., Sakai N., Al Ashkel A., Feldman D.;
 RT "A novel mutation in the deoxythymine acid-binding domain of the
 RT vitamin D receptor causes hereditary 1,25-dihydroxyvitamin D-resistant
 RT rickets."
 RL J. Clin. Endocrinol. Metab. 81:2564-2569(1996).
 RN [14]
 RP VAPJANIS 310 314 AND 310 391;
 RX MEDLINE 97126600; PubMed 8961271;
 RA Whitfield G.K., Selznick S.H., Bussler C.A., Bush J.,
 RA Galligan M.A., Jurek P.W., Thompson P.D., Lee S.M., Zerkow J.E.,
 RA Bussler M.R.;
 RT "Vitamin D receptors from patients with resistance to 1,25-
 RT dihydroxyvitamin D(3): point mutations confer reduced transactivation
 RT in response to ligand and impaired interaction with the retinoid X
 RT receptor heterodimeric partner."
 RL Mol. Endocrinol. 10:1617-1631(1996).
 RN [15]
 RP VAPJANIS 310 405;
 RX MEDLINE 97158638; PubMed 9005998;
 RA Malloy P.J., Kesterson R.A., Gross C., van Maldergem L., Bouillon R.,
 RA Feldman D.;
 RT "Hereditary vitamin D resistant rickets caused by a novel mutation in
 RT the vitamin D receptor that results in decreased affinity for hormone
 RT and cellular responsiveness."
 RL J. Clin. Invest. 99:297-304(1997).
 RN [16]
 RP PDB: 1VOR;
 RT "THE EXPRESSION OF HORMONE-SENSITIVE GENES."
 RT "SIGNALING INTERACTIONS WITH SMAD3."
 RT "SUBCELLULAR LOCATION: NUCLEAR."
 RT "DOMAIN: COMPOSED OF THREE DOMAINS: A REGULATING N-TERMINAL DOMAIN,
 RT A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN."
 RT "DISEASE: DEFECTS IN VOR ARE THE CAUSE OF TYPE IIA RICKETS (AIRS).
 RT KNOWN AS: HYPOCALCAEMIC VITAMIN D RESISTANT RICKETS (HVDR). HVDR
 RT IS MOST FREQUENTLY AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED
 RT BY SEVERE RICKETS, HYPOCALCAEMIA AND SECONDARY HYPERPARATHYROIDISM.
 RT SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 RT NOT SUBMITTAL.
 RT "CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-4 IS THE INITIATOR.
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 RT between the Swiss Institute of Bioinformatics and the EMBL outstation
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 RT use by non-profit institutions as long as its content is in no way
 RT modified and this statement is not removed, misused, or for commercial
 RT purposes. Send an email to license@sb-ethb.ch."
 RN [17]
 RP EMBL: J03258; AAA61273.1;
 RN [18]
 RP EMBL: X67482; CAA47824.1;
 RN [19]
 RP EMBL: AF028260; AAR95155.1;
 RN [20]
 RP EMBL: AB002168; BAA4389.1;
 RN [21]
 RP EMBL: AB002161; BAA4389.1; J01NE0;
 RN [22]
 RP EMBL: AB002162; BAA4389.1; J01NE0;
 RN [23]
 RP EMBL: AB002163; BAA4389.1; J01NE0;
 RN [24]
 RP EMBL: AB002164; BAA4389.1; J01NE0;
 RN [25]
 RP EMBL: AB002165; BAA4389.1; J01NE0;
 RN [26]
 RP EMBL: AB002166; BAA4389.1; J01NE0;
 RN [27]
 RP EMBL: AB002167; BAA4389.1; J01NE0;
 RN [28]
 RP EMBL: M65208; AAA61274.1;
 RN [29]
 RP PIR: A28200; A28200;
 RN [30]
 RP PIR: S24174; S24174;
 RN [31]
 RP DSSP: P04722; TRQ;
 RN [32]
 RP TRANSFAC: T08885;
 RN [33]
 RP MIM: 601769;
 RN [34]
 RP MIM: 277440;
 RN [35]
 RP InterPro: IPR01628; 21-64;
 RN [36]
 RP Pfam: PF00104; hormone_rec; 1;
 RN [37]
 RP Pfam: PF00105; 21-64; 1;

DR PRINTS: PR00047: STROJDINGER.
 DR PRINTS: PR00560: VITAMINDR.
 DR SMART: SM00430: H011: 1.
 DR SMART: SM00399: ZNF_C4: 1.
 DR PROSITE: PS00041: NUCLEAR_RECEPTOR; 1.
 DR Receptor: Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; phosphorylation; Disease mutation.
 FT DNA_BIND 24 89 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 24 44 C4-TYPE.
 FT ZN_FING 60 84 C4-TYPE.
 FT DOMAIN 90 191 HINGE.
 FT DOMAIN 192 427 LIGAND-BINDING.
 FT VARIANT 33 33 G -> D (IN RICKETS).
 FT VARIANT 35 35 /FTID=VAR_004656.
 FT VARIANT 45 45 H -> Q (IN RICKETS).
 FT VARIANT 45 45 K -> E (IN RICKETS).
 FT VARIANT 46 46 G -> D (IN RICKETS).
 FT VARIANT 47 47 F -> I (IN RICKETS).
 FT VARIANT 50 50 /FTID=VAR_004660.
 FT VARIANT 50 50 R -> Q (IN RICKETS).
 Query Match 44.3%; Score 750; DR 1; Length 427;
 Best Local Similarity 40.3%; Pred. No. 2,86-53;
 Matches 166; Conservative 62; Mismatches 136; Indels 48; Gaps 8;

QY 48 PQLGVGCAKAGVHFNMTGEGKGFPRKAMKRNARLRCFPRKACETITKTRCOAC 97
 DB 21 PRICGVGCAKAGVHFNMTGEGKGFPRKAMKRNARLRCFPRKACETITKTRCOAC 97
 QY 98 RLKRLTESGMMKEMMSDFAEVERBALIKRKSEPTGTPGLGVGLTEQYMMIRELMDA 157
 DB 80 RLKRLTESGMMKEMMSDFAEVERBALIKRKSEPTGTPGLGVGLTEQYMMIRELMDA 157
 QY 158 QMKITDTFESHKRNKRLPGVLSQ-----CPLPESLQAPRSREAKMSQVRKDC----- 207
 DB 139 HKRTDTPYSDFCOFPRPVKYNDDGSGHPSRNSHHPS--FSGDSSSSSCHCTTSSDM 196
 QY 208 ---SIKVSLSLQGEDEGSVWNNKFPADSGKKEFSLPPHADMSTYFKGIIISFAKVISYF 264
 DB 197 MSSSFSNLDISEEDSD-----DPSVITLIELSQLPHLADIVSISLQKVIQFAMMIGCF 251
 QY 265 RQLPTEIDISLKGAFELQURENTVNAETGWEGRSY---CLPDINGGVOQLLE 321
 DB 252 RQLPTEIDISLKGAFELQURENTVNAETGWEGRSY---CLPDINGGVOQLLE 321
 QY 372 PMLKRYHMLKRIQLHEEYVIMQALISLSPDRPVAVLOHVVUOLQOFAITLKSYIEGNR 381
 DB 372 PMLKRYHMLKRIQLHEEYVIMQALISLSPDRPVAVLOHVVUOLQOFAITLKSYIEGNR 381
 QY 382 PPARFLFLIKIMMILEF-----ATPDMELFG 410
 DB 372 PTPGSHLLYAKMKICKLADLSINERHSKQYRCISFQPECSMKLTPLVLEVIG 423

RESULT 11
 NR13_HUMAN
 ID NR13_HUMAN STANDARD; PRT: 348 AA.
 AC Q14994;
 DT 15-JUL-1999 (rel. 38, Created)
 DT 15-JUL-1999 (rel. 38, last sequence update)
 DT 20-AUG-2001 (rel. 40, last annotation update)
 DE ORPHAN NUCLEAR RECEPTOR NR13 (CONSTITUTIVE ANDROSTANE RECEPTOR) (CAR)
 DE (ORPHAN NUCLEAR RECEPTOR NR67).
 GN NR13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.

KC TISSUE: LIVER;
 KX MEDLINE:94158827; PubMed:8114692;
 RA Baes M., Gulick L., Choi H.S., Martinoli M.G., Simha D., Moore D.D.;
 RT "A new orphan member of the nuclear hormone receptor superfamily that
 RT interacts with a subset of retinoic acid response elements.";
 RL Mol. Cell. Biol. 14:1544-1552(1994).
 CC -1- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
 CC ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR
 CC BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES. TRANSACTIVATES BOTH THE
 CC PHENOBARBITAL RESPONSIVE ELEMENT MODULE OF THE HUMAN CYP2B6 GENE
 CC AND THE CYP3A4 XENOBOTIC RESPONSE ELEMENT.
 CC -1- SUBUNIT: HETERODIMER OF NR13 AND RXR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
 CC -1- INDUCTION: BY DEXAMETHASONE.
 CC -1- DOMAIN: COMPOSED BY A SHORT N-TERMINAL DOMAIN FOLLOWED BY THE DNA
 CC BINDING, HINGE, AND LIGAND BINDING/DIMERIZATION DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR1 SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z10425; CAA83016.1; -;
 DR MIM: 603881; -;
 DR InterPro: IP000536; Hormone_rec_114.
 DR InterPro: IP001628; ZF-C4.
 DR Pfam: PF00104; hormone_rec_1.
 DR Pfam: PF00105; ZF-C4; 1.
 DR PRINTS: PR00047: STROJDINGER.
 DR PRINTS: PR00350: VITAMINDR.
 DR PRINTS: PR00560: VITAMINDR.
 DR SMART: SM00430: H011: 1.
 DR SMART: SM00399: ZNF_C4: 1.
 DR PROSITE: PS00041: NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Activator.
 FT DNA_BIND 11 76 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 11 31 C4-TYPE.
 FT ZN_FING 47 71 C4-TYPE.
 FT ZN_FING 47 71 C4-TYPE.
 SQ SEQUENCE 348 AA; 39558 MW; 92FAAD07D70C90A CRC64;

Query Match 44.3%; Score 741; DR 1; Length 448;
 Best Local Similarity 40.5%; Pred. No. 7,46-72;
 Matches 157; Conservative 59; Mismatches 100; Indels 72; Gaps 6;

QY 41 CAVGQDKATGVHFNMTGEGKGFPRKAMKRNARLRCFPRKACETITKTRCOAC 100
 DB 11 CAVGQDKATGVHFNMTGEGKGFPRKAMKRNARLRCFPRKACETITKTRCOAC 100
 QY 101 KLESQMKKEMMSDEAVEERBALIKRKSEPTGTPGLGVGLTEQYMMIRELMDA 160
 DB 70 KLDQCKMKRMTLSAFALIRAKQOGBRAQVTVV---LSKDFELLRIITLHMT 124
 QY 161 TFDITFSHKRNKRLPGVLSGCELPESLQASREFAKMSQVRKDC/SIKVSLSLQGEDE 220
 DB 124 HMGTFEFGVFRPAPHFHHQ-PLPTLAD----- 154
 QY 221 SVMWKRPAVDSGKEFSLPPHADMSTYFKGIIISFAKVISYFQPLTEQYSLKGA 280
 DB 154 -----VLPLVTHPADINPMVLQVTKRLPVKRSIPTRQSLKGA 198
 QY 281 FELQURENTVNAETGWEGRSYCLQEDTAG-GFOQLLEPMKRYMMLKRIQLHEE 349
 DB 199 VELQIVNTITFCIQTFGLGPLEKYTEEDGARVGVVERLELDLPHRGLIKRIQDE 258
 QY 340 VLMQALISLSPDRPVAVLOHVVUOLQOFAITLKSYIEGNRQVPAIRFLFLIKIMMILE 499

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF009427; AAC53434.1; -;
 DR EMBL: AF009428; AAC53450.1; -;
 DR MGI: MGI:1446407; Nr113.
 DR InterPro: IPR000546; Hormone_rec_119.
 DR InterPro: IPR001723; Steroidhormone_receptor.
 DR InterPro: IPR001628; z1-c4.
 DR Pfam: PF00104; hormone_rec1.
 DR Pfam: PF00105; z1-c4.1.
 DR PRINTS: PR00047; STROLOPFINGR.
 DR PRINTS: PR00150; VITAMINR.
 DR PRINTS: PR00398; STROHOMNR.
 DR PRINTS: PR00546; HYROIDHOMR.
 DR SMART: SM00430; HOL1.1.
 DR SMART: SM00499; Znf_C4.1.
 DR Pfam: PF00031; NUCLEAR_RECEPTOR_1.
 DR KEGG: K01199; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc finger; Activator; Alternative splicing.
 FT DNA_BIND 21 86
 FT ZN_FING 21 41
 FT ZN_FING 57 81
 FT VARSPLIC 281 286
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Genome version 4.5
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OM protein - protein search, using sw model

Run on: March 2, 2002, 02:38:10 ; Search time 56.22 seconds

(without alignments)
1077.139 Million cell updates/sec

Title: US-09-276-935b-14
Perfect score: 2187
Sequence: 1 LEVRFKESNMHAFVCEET.....AMLEFATPLMQHLEFQITGS 414

Scoring table:
HUSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 08
FastDB-Title 45 summaries

Database : SPTREPM01_17 :
1: SP-archaea :
2: SP-bacteria :
3: SP-fungi :
4: SP-human :
5: SP-invertebrate :
6: SP-mammal :
7: SP-mhc :
8: SP-organelle :
9: SP-plant :
10: SP-plant :
11: SP-rodent :
12: SP-virus :
13: SP-vertebrate :
14: SP-unclassified :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2167	99.1	473	4	Q9UNM4
2	2158	98.7	457	4	Q9UNM6
3	2156	98.6	434	4	Q9UNJ27
4	1948.5	88.6	420	4	Q9UNJ23
5	1946.5	88.5	397	4	Q9UNJ24
6	1851	84.6	479	4	Q9UNJ25
7	1700.5	77.8	411	6	Q9UNJ22
8	1631.5	74.6	342	4	Q9UNJ22
9	922.5	42.2	386	13	Q9UNJ39
10	922.5	42.2	388	13	Q9UNJ24
11	876.5	40.1	391	13	Q9UNJ24
12	771	35.3	420	13	Q9UNJ23
13	748.5	34.2	425	13	Q9UNJ24
14	746	34.1	453	13	Q9UNJ22
15	546.5	24.5	124	11	Q9UNJ20
16	453	20.7	518	5	Q9UNJ26
17	444.5	19.9	784	5	Q9UNJ26
18	431	19.7	673	5	Q9UNJ26
19	428.5	19.6	680	5	Q9UNJ24

20	424.5	19.4	472	4	Q9UNJ43
21	413.5	18.9	881	5	Q9UNJ38
22	411	18.8	469	11	Q62735
23	410.5	18.8	541	5	Q97095
24	406.5	18.6	484	11	Q60641
25	402.5	18.4	491	5	Q02045
26	401	18.3	454	13	Q9UNJ24
27	393	18.0	447	13	Q9UNJ23
28	390.5	17.9	457	13	Q9UNJ22
29	387.5	17.7	444	5	Q44336
30	387	17.7	560	5	Q44337
31	387	17.7	570	5	Q44338
32	386	17.6	444	13	Q9UNJ21
33	386	17.6	444	13	Q9UNJ21
34	385.5	17.6	513	5	Q77240
35	385.5	17.6	541	5	Q77245
36	384	17.6	455	13	Q9UNJ43
37	383	17.5	459	11	Q9UNJ11
38	382.5	17.5	452	13	Q9UNJ55
39	381	17.4	367	13	Q9UNJ23
40	381	17.4	448	13	Q9UNJ19
41	381	17.4	555	12	Q9UNJ54
42	378	17.3	455	12	Q85511
43	378	17.3	555	12	Q46200
44	378	17.3	582	12	Q9UNJ53
45	375	17.1	453	13	Q9UNJ67

ALIGNMENTS

RESULT	ID	Q9UNM4	PRELIMINARY	PRG	473 AA
AC	Q9UNM4				
DT	01-MAY-2000	(TEMBLE1.13, created)			
DT	01-MAY-2000	(TEMBLE1.13, last sequence update)			
DT	01-JUN-2001	(TEMBLE1.17, last annotation update)			
DE	ORPHAN NUCLEAR RECEPTOR.				
GN	PAR2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RX	MEDLINE-98445350; PubMed-970465;				
RA	Bertilsson G., Heidrich J., Svensson K., Asman M., Jendelberg L.,				
RA	Sydow Backman M., Ohlsson K., Postlund H., Nilsson J.,				
RA	Berkstrand A.,				
RT	*Identification of a human nuclear receptor defines a new signaling				
RT	pathway for CYP3A induction.*				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:12208-12214(1998).				
CC	-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.				
CC	EMBL: AF084644; AAC64557.1; -				
DR	HSSP: P10826; IIRK.				
DR	InterPro: IPR000546; Hormone_Rec_114.				
DR	InterPro: IPR001723; Steroidhormone_receptor.				
DR	InterPro: IPR001628; Z1-C4.				
DR	Pfam: PF00104; Hormone_rec_1.				
DR	Pfam: PF00105; Z1-C4; 1.				
DR	PRINTS: PR00398; STRODOHOMER.				
DR	PRINTS: PR00047; STRODOHOMER.				
DR	SMART: SM00430; B01.1.				
DR	SMART: SM00399; Z0F-C4; 1.				
DR	PROSITE: PS00041; NUCLEAR-RECEPTOR; 1.				
KW	LAM-binding; Nuclear protein; Receptor; Transcription regulation;				
KW	Zinc-finger.				
SO	SEQUENCE 473 AA; 54899 MW; 4049029098403016 GC%64;				

Query Match 99.98% Score 216/216 Pos 4 Length 474
 Host Local Similarity 95.48% Pos. No. 60-179
 Match 414 Conserved 0 Mismatches 0 Indels 20 Gaps 1

1 LEVGRKESNMADVEVHEDTESVYKSKSVNADDEWVQVGRVGRKATGYHNVMTG 60
 40 LEVGRKESNMADVEVHEDTESVYKSKSVNADDEWVQVGRVGRKATGYHNVMTG 99
 61 CKGPRKAMKRNALRQYERKCAELETTRKTRQCVATRLKRLKESKREKIMSDFAVE 120
 100 CKGPRKAMKRNALRQYERKCAELETTRKTRQCVATRLKRLKESKREKIMSDFAVE 159
 121 KRALIKRKSRPTQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 180
 160 KRALIKRKSRPTQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 219
 181 GPELPESIGASREFAKWSQVRKIDSLKVSQVGRKESVNNKTPVANSCKEETSL 240
 220 GPELPESIGASREFAKWSQVRKIDSLKVSQVGRKESVNNKTPVANSCKEETSL 279
 241 PHMAIMSYMEKGLISPAKVSFGRDPTEDQSLKGAAPLQVLRNIVNAGETWE 300
 260 PHMAIMSYMEKGLISPAKVSFGRDPTEDQSLKGAAPLQVLRNIVNAGETWE 339
 301 CGRLSYLQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 369
 340 CGRLSYLQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 399
 361 VVGLQVDPFATLKSYTEFNQVAFHRLPKIMAMLE 400
 400 VVGLQVDPFATLKSYTEFNQVAFHRLPKIMAMLE 439
 401 ATPMOEFCTGS 414
 440 ATPMOEFCTGS 474

RESULT 2
 Q90126 PRELIMINARY PRT: 457 AA.

01 MAY 2000 (TEMPREL: 13, created)
 01 MAY 2000 (TEMPREL: 13, last sequence update)
 01 JUN 2001 (TEMPREL: 17, last annotation update)
 NUCLEAR HORMONE RECEPTOR PRK1 C.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartida; Homidae; Homo.
 NCBI TaxID 9606.
 SEQUENCE FROM N.A.
 TISSUE LIVER.
 Heard D.J., Holloway J., Hansen C., Fawcett N., Axford L.,
 *Identification of a novel protein isoform of the human nuclear
 hormone receptor RXR/SXR and localization to chromosome 4q12.1
 13.3.
 Eur. J. Hum. Genet. 0:0-0(0).
 1. SIMILARITY TO C4 TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 EMO: A0009406; CA055490.1.
 HSSB: P10826; IIRK.
 InterPro: IPR000546; Hormone rec 13.
 InterPro: IPR001243; Steroid hormone receptor.
 InterPro: IPR001628; ZF C4.
 Pfam: Pfam0404; Hormone rec 1.
 Pfam: Pfam0404; Hormone rec 1.
 PRINTS: PR00490; SKR000000.
 PRINTS: PR00472; STK000000.
 SMART: SM00400; HNF1.
 SMART: SM00400; ZNF C4.
 ProSITE: PS00105; NUCLEAR RECEPTOR 1.

KW DNA binding; Nuclear protein; Receptor; Transcription regulator;
 KW Zinc finger.
 SW SEQUENCE 457 AA: 52145 MW: 81268.6457046 E08064

Query Match 98.78% Score 2158/2160 Pos 4 Length 457
 Host Local Similarity 94.78% Pos. No. 4-178
 Match 412 Conserved 0 Mismatches 2 Indels 20 Gaps 1

1 LEVGRKESNMADVEVHEDTESVYKSKSVNADDEWVQVGRVGRKATGYHNVMTG 60
 24 LEVGRKESNMADVEVHEDTESVYKSKSVNADDEWVQVGRVGRKATGYHNVMTG 84
 61 CKGPRKAMKRNALRQYERKCAELETTRKTRQCVATRLKRLKESKREKIMSDFAVE 120
 84 CKGPRKAMKRNALRQYERKCAELETTRKTRQCVATRLKRLKESKREKIMSDFAVE 144
 121 KRALIKRKSRPTQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 160
 144 KRALIKRKSRPTQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 203
 181 GPELPESIGASREFAKWSQVRKIDSLKVSQVGRKESVNNKTPVANSCKEETSL 240
 204 GPELPESIGASREFAKWSQVRKIDSLKVSQVGRKESVNNKTPVANSCKEETSL 264
 241 PHMAIMSYMEKGLISPAKVSFGRDPTEDQSLKGAAPLQVLRNIVNAGETWE 300
 264 PHMAIMSYMEKGLISPAKVSFGRDPTEDQSLKGAAPLQVLRNIVNAGETWE 324
 301 CGRLSYLQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 360
 324 CGRLSYLQVGLVQVGLTFEYGRMMRELMDAMKTEPTESHKRNPVYSS 384
 361 VVGLQVDPFATLKSYTEFNQVAFHRLPKIMAMLE 400
 384 VVGLQVDPFATLKSYTEFNQVAFHRLPKIMAMLE 444
 401 ATPMOEFCTGS 414
 444 ATPMOEFCTGS 457

RESULT 3
 Q90127 PRELIMINARY PRT: 444 AA.

01 MAY 2000 (TEMPREL: 13, created)
 01 MAY 2000 (TEMPREL: 13, last sequence update)
 01 JUN 2001 (TEMPREL: 17, last annotation update)
 NUCLEAR HORMONE RECEPTOR PRK1 A.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartida; Homidae; Homo.
 NCBI TaxID 9606.
 SEQUENCE FROM N.A.
 TISSUE LIVER.
 Heard D.J., Holloway J., Hansen C., Fawcett N., Axford L.,
 *Identification of a novel protein isoform of the human nuclear
 hormone receptor RXR/SXR and localization to chromosome 4q12.1
 13.3.
 Eur. J. Hum. Genet. 0:0-0(0).
 1. SIMILARITY TO C4 TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 EMO: A0009406; CA055489.1.
 HSSB: P10826; IIRK.
 InterPro: IPR000546; Hormone rec 13.
 InterPro: IPR001243; Steroid hormone receptor.
 InterPro: IPR001628; ZF C4.
 Pfam: Pfam0404; Hormone rec 1.
 Pfam: Pfam0404; Hormone rec 1.

DR PRINTS: PR003498; STRDHOMNER.
 DR PRINTS: PR000447; STROLDINGER.
 DR SMART: SM00440; HOL: 1.
 DR SMART: SM00399; ZOF_C4: 1.
 DR PRINTS: PR00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding: Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SW SEQUENCE: 414 AA; 49777 MW; AB360C28C4C200 CIRC64;

Query Match 98.6%; Score 2156; DB 4; Length 434;
 Best Local Similarity 94.7%; Pred. No. 4, 8e-178;
 Matches 411; Conservative 1; Mismatches 2; Indels 20; Gaps 1;

QY 1 LEVRKESNNIADPHVCHDTSVPKPSVNADEVGQICRVGDKATGYHFWMTGEG 60
 DB 1 MEVRKESNNIADPHVCHDTSVPKPSVNADEVGQICRVGDKATGYHFWMTGEG 60
 QY 61 CKGFFRANKRNARLCPFRKACETTRKTRQCAACRLKCLSGSKKEMISDAVEE 120
 DB 61 CKGFFRANKRNARLCPFRKACETTRKTRQCAACRLKCLSGSKKEMISDAVEE 120
 QY 121 RRALLKRRKSEPTGTPLGVGLTEBQRMIRLMDAOKTFDTTFSEKNEFLGVLS 180
 DB 121 RRALLKRRKSEPTGTPLGVGLTEBQRMIRLMDAOKTFDTTFSEKNEFLGVLS 180
 QY 181 GGLPESLIQAPSRFAAKSVKRLDLSKVSLOLRGEGSVWYKPPRDSGKEFLSL 240
 DB 181 GGLPESLIQAPSRFAAKSVKRLDLSKVSLOLRGEGSVWYKPPRDSGKEFLSL 240
 QY 241 PHMAIMSTYMKGLISPAKVISYFRDLPEDQISLKGAARLQURNTVNAETGWE 300
 DB 241 PHMAIMSTYMKGLISPAKVISYFRDLPEDQISLKGAARLQURNTVNAETGWE 300
 QY 301 CGRLSYCEDIAGCPDOLLLEPMLKFNHMKKIQLHEEYVLMQATSLFSPRPVLOHR 360
 DB 301 CGRLSYCEDIAGCPDOLLLEPMLKFNHMKKIQLHEEYVLMQATSLFSPRPVLOHR 360
 QY 361 VVDUQEQPATLTKSYTECNRPQPAHREFLKIMMLTE-----F 400
 DB 361 VVDUQEQPATLTKSYTECNRPQPAHREFLKIMMLTE-----F 400
 QY 401 ATPMDELFGITGS 414
 DB 401 ATPMDELFGITGS 434
 RESULT 4
 Q90J23 PRELIMINARY: PRT: 420 AA.
 ID Q90J23:
 DT 01-MAY-2000 (Tremblérel, 13, Created)
 DT 01-MAY-2000 (Tremblérel, 13, Last sequence update)
 DT 01-JUN-2001 (Tremblérel, 17, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRR2-C.
 CN PRR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC TISSUE: LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT *Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PXR/SXR and localization to chromosome 3q12.1
 RT -13.3.*;
 RL Eur. J. Hum. Genet. 0:0-0(0).
 CC -1- SIMILARITY: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR PMID: A000937; CAB5493.1;
 DR HSP; P10826; 1HRA.

DR InterPro: IPR000536; Hormone_rec_13.
 DR InterPro: IPR001723; Steroid_hormone_receptor.
 DR InterPro: IPR001628; Z1_C4.
 DR Pfam: PF00104; Hormone_rec_1.
 DR Pfam: PF00105; Z1_C4.
 DR PRINTS: PR003498; STRDHOMNER.
 DR PRINTS: PR000447; STROLDINGER.
 DR SMART: SM00440; HOL: 1.
 DR SMART: SM00399; ZOF_C4: 1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding: Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SW SEQUENCE: 420 AA; 48149 MW; CP4D9E156859165 CIRC64;

Query Match 88.6%; Score 1938.5; DB 4; Length 420;
 Best Local Similarity 86.4%; Pred. No. 2, 8e-199;
 Matches 375; Conservative 0; Mismatches 2; Indels 57; Gaps 2;

QY 1 LEVRKESNNIADPHVCHDTSVPKPSVNADEVGQICRVGDKATGYHFWMTGEG 60
 DB 24 LEVRKESNNIADPHVCHDTSVPKPSVNADEVGQICRVGDKATGYHFWMTGEG 84
 QY 61 CKGFFRANKRNARLCPFRKACETTRKTRQCAACRLKCLSGSKKEMISDAVEE 120
 DB 84 CKGFFRANKRNARLCPFRKACETTRKTRQCAACRLKCLSGSKKEMISDAVEE 143
 QY 121 RRALLKRRKSEPTGTPLGVGLTEBQRMIRLMDAOKTFDTTFSEKNEFLGVLS 180
 DB 144 RRALLKRRKSEPTGTPLGVGLTEBQRMIRLMDAOKTFDTTFSEKNEFLGVLS 196
 QY 181 GGLPESLIQAPSRFAAKSVKRLDLSKVSLOLRGEGSVWYKPPRDSGKEFLSL 240
 DB 197 -----VSLOLRGEGSVWYKPPRDSGKEFLSL 226
 QY 241 PHMAIMSTYMKGLISPAKVISYFRDLPEDQISLKGAARLQURNTVNAETGWE 300
 DB 227 PHMAIMSTYMKGLISPAKVISYFRDLPEDQISLKGAARLQURNTVNAETGWE 286
 QY 301 CGRLSYCEDIAGCPDOLLLEPMLKFNHMKKIQLHEEYVLMQATSLFSPRPVLOHR 360
 DB 287 CGRLSYCEDIAGCPDOLLLEPMLKFNHMKKIQLHEEYVLMQATSLFSPRPVLOHR 346
 QY 361 VVDUQEQPATLTKSYTECNRPQPAHREFLKIMMLTE-----F 400
 DB 347 VVDUQEQPATLTKSYTECNRPQPAHREFLKIMMLTE-----F 400
 QY 401 ATPMDELFGITGS 414
 DB 407 ATPMDELFGITGS 420
 RESULT 5
 Q90J24 PRELIMINARY: PRT: 397 AA.
 ID Q90J24:
 DT 01-MAY-2000 (Tremblérel, 13, Created)
 DT 01-MAY-2000 (Tremblérel, 13, Last sequence update)
 DT 01-JUN-2001 (Tremblérel, 17, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRR2-A.
 CN PRR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID 9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC TISSUE: LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT *Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PXR/SXR and localization to chromosome 3q12.1
 RT -13.3.*;

RC STRAIN BREED NEW ZEALAND WHITE RABBIT; ISSUE KIDNEY;


```

BI 01-JUN-2001 (TRENDEL, 17, created)
DT 01-JUN-2001 (TRENDEL, 17, last sequence update)
DT 01-JUN-2001 (TRENDEL, 17, last annotation update)
DE NOCLEAR RECEPTOR SUBFAMILY 1, GROUP 1, MEMBER 2 (FRAGMENT).
CN NR112.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN 111)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX MEDLINE:21085660; PubMed:11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kuno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori I., Hono H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King H., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole C., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Norone P., Ringwald M., Rodriguez L., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Welter G., Whitaker C., Wilming L.,
RA Wyshaw-Borja A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RA "National annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001);
RC -1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY);
CC -1 SIMILARITY: to C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL: AK011108; BAB27404.1;
DR MGI: MGI:1437040; Nr112.
DR TrEMBL: P0001628; ZF-C4.
DR PIR: P00105; ZF-C4.1.
DR PRINTS: P000047; STERIODFINGER.
DR SMART: SM00399; ZNF_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc finger.
PT NON_TER 124 124
SQ SEQUENCE 124 AA: 1433 MW: 2183434248661 CQC64;

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Query Match 24.5%; Score 536.5; DB 11; Length 124;
 Best Local Similarity 78.4%; Pred. No. 7e-39;
 Matches 98; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

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QY 4 VRPESMNNAHVEVCHDTSVPGKPSVNDPEVGGPQICVAGD30KAIQYHFNMTCEGCK 62
DB 1 MRFEESSMSKVGVLQCEADSALEEP-INVFEHGGSLQICRVGCDKANGHFNMTCEGCK 59
QY 63 GFFRRAMKRNARIKPFRRQACELTKIRQCACRIKKCLSGMKKEMIMSDAVERRR 122
DB 60 GFFRRAMKRNVRIRPFRRQTCETIKTKTRQACRIKKCLSGMKKEMIMSDAVERRR 119
QY 123 ALIKR 127
DB 120 ALIKR 124

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Search completed: March 2, 2002, 02:44:32
 Job time: 382 sec

SeqCore version 4.5
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OM nucleotide - nucleotide search, using sw model

Run on: March 2, 2002, 00:47:14 : Search time 2115.04 Seconds
(without alignments)

16738.666 Million cell updates/sec

Title: US-09-276-935B-13

Sequence: 1 tgaattatataaqqtaaaqaaacaa.....aaqtaataaaatataatctaaq 2146

Scoring table: IDENTITY-MTC

Gapop 10.0, Gapext 1.0

Searched: 1472140 sweeps, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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35: gb_bg.*
36: gb_bg.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2146	100.0	2146	AF061056	AF061056 Homo sapi
2	2128.6	99.2	4448	HSAB1936	HSAB1936 Homo sapi
3	2115.4	98.6	4057	E32709	E32709 Novel nucle
4	2086.2	97.2	2905	AF084645	AF084645 Homo sapi
5	2006.6	94.5	4244	E32708	E32708 Novel nucle
6	1896.6	88.4	4347	HSAB1937	HSAB1937 Homo sapi
7	1866.6	87.0	2802	AF084644	AF084644 Homo sapi
8	1741.2	81.1	2068	AX172810	AX172810 Sequence
9	1374	64.0	1374	E32701	E32701 Novel nucle
10	1330.2	62.0	1422	E32702	E32702 Novel nucle
11	1305	60.8	1305	E32700	E32700 Novel nucle
12	1101	51.3	1895	AF182217	AF182217 Cytochal
13	1006.8	46.9	1709	AF031814	AF031814 Mus musc
14	1003.2	46.7	1755	AF151377	AF151377 Batifus to
15	991.4	46.2	1601	AF188476	AF188476 Cytochal
16	746.6	44.3	801	AF129253	AF129253 Sequence
17	682.4	41.8	86081	AF064606	AF064606 Homo sapi
18	682.4	41.8	100185	AC069444	AC069444 Homo sapi
19	608.2	28.3	644	E32706	E32706 Novel nucle
20	284	13.2	1340	AF2276753	AF2276753 Batifus to
21	280.8	13.1	1377	MUSVDR	MUSVDR Mus musc
22	280.8	13.1	3328	10	BC006716
23	279.4	13.0	3315	AY007189	AY007189 Homo sapi
24	279	13.0	962	AX137046	AX137046 Sequence
25	278.8	13.0	2043	RA189VDR3	RA189VDR3 Sequence
26	278.2	13.0	962	AX099115	AX099115 Sequence
27	277.2	12.9	415	AX137054	AX137054 Sequence
28	276.8	12.9	415	AX099119	AX099119 Sequence
29	276.4	12.9	1790	AF052201	AF052201 Xenopus l
30	275	12.8	2494	AF011356	AF011356 Galinus ga
31	272.8	12.7	1284	AX151193	AX151193 Sequence
32	272.8	12.7	1284	AF026260	AF026260 Homo sapi
33	272.8	12.7	1335	HSVDR	HSVDR Human vitam
34	272.8	12.7	4604	HUMVDR	HUMVDR Human vitam
35	267.8	12.5	1724	CJ012641	CJ012641 Corchorus ja
36	264.8	12.3	1284	AF354232	AF354232 Sequins
37	258.6	12.1	1638	AX137060	AX137060 Sequence
38	243.6	11.4	324	AX099122	AX099122 Sequence
39	242.8	11.3	324	AB037674	AB037674 Homo sapi
40	239.8	11.2	2429	AF164512	AF164512 Homo sapi
41	236.6	11.0	1503	E14584	E14584 Batifus to
42	236	11.0	1071	E14584	E14584 Batifus to
43	232	10.8	1782	AX037673	AX037673 Paratich
44	230.4	10.7	2659	5	AX137048
45	222	10.3	345	6	AX137048

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS
AF061056	AF061056	Homo sapiens orphan nuclear receptor PKR mRNA, complete cds.	AF061056	AF061056.1	GI:3511137	human	Homo sapiens	The human orphan nuclear receptor PKR is activated by compounds that regulate CYP3A4 gene expression and cause drug interactions	J. Clin. Invest. 102 (5), 1016-1024 (1998)	98395174	2 (bases 1 to 2146)	Lehmann, J.M., McKee, D.D., Watson, M.A., Willson, T.M., Moore, J.T. and

[illegible][illegible]

[illegible][illegible]

[illegible][illegible]

Sat Mar 2 12:27:38 2002

us-09-276-935b-13.rge

Page

Genome version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 00:48:49 ; Search time 139.68 Seconds
(without alignments)
13171.678 Million cell updates/sec

Title:

08-09-276-935b-13

Perfect score:

2146

Sequence: 1 tgaatataatgagagagca.....aaatgcatgagatctgag 2146

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:

940621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2146	100.0	2146	AAZ07997	Human pregnane X r
2	2115.4	98.6	3057	AAZ59975	DNA encoding an in
3	2101.4	97.9	4093	AAZ78807	Human nNRT cDNA.
4	2075.2	96.7	2910	AAZ56242	Human vitamin D re
5	2006.4	93.5	4243	AAZ59974	DNA encoding an in
6	1866.6	87.0	2802	AAZ56243	Human vitamin D re
7	1866.6	87.0	2850	AAZ78808	Human nNRT-1 cDNA.
8	1744.4	81.3	2068	AAZ89080	Human steroid and
9	1744.4	81.3	2068	AAZ89080	Nucleotide sequen
10	1474	64.0	20	AAZ59967	DNA encoding an in
11	1330.2	62.0	20	AAZ59968	DNA encoding an in

12	1305	60.8	1305	20	AAZ59966	DNA encoding an in
13	736.6	34.3	801	22	AAZ80601	Receptor *49 part I
14	608.2	28.3	644	20	AAZ59972	Seq ID 12 of JP111
15	599.2	27.9	711	22	AAZ44900	Human cytochrome
16	278.8	13.0	1960	19	AAZ01129	cDNA encoding rat
17	278.8	13.0	2043	14	AAZ01425	Kat vitamin D rece
18	278.2	13.0	962	22	AAZ02902	Human pregnane X r
19	276.8	12.9	415	22	AAZ02906	Human pregnane X r
20	272.8	12.7	1284	22	AAZ24801	Nucleotide sequen
21	272.8	12.7	1382	20	AAZ44789	Nucleotide sequen
22	272.8	12.7	1463	20	AAZ44788	Nucleotide sequen
23	272.8	12.7	1574	20	AAZ44793	Nucleotide sequen
24	272.8	12.7	3510	20	AAZ02945	Human vitamin D re
25	272.8	12.7	4604	19	AAZ1327	Human vitamin D re
26	271.2	12.6	1899	14	AAZ01424	Human vitamin D re
27	264.2	12.3	300	22	AAZ44484	Human cytochrome
28	257	12.0	2191	17	AAZ64499	Xenopus cytochrome
29	242.8	11.3	324	22	AAZ02909	Human pregnane X r
30	236	11.0	1071	20	AAZ16596	Kat vitamin D rece
31	236	11.0	3382	19	AAZ18518	cDNA encoding rat
32	236	11.0	3382	20	AAZ16606	Kat vitamin D rece
33	220.8	10.3	345	22	AAZ02903	Human pregnane X r
34	220.4	10.3	345	22	AAZ02896	DNA encoding human
35	220.4	10.3	345	22	AAZ02897	DNA encoding human
36	220.4	10.3	345	22	AAZ02898	DNA encoding human
37	215	10.0	1534	20	AAZ44790	Nucleotide sequen
38	186.6	8.8	1404	20	AAZ16597	Human vitamin D re
39	188.4	8.8	423	22	AAZ02905	Human pregnane X r
40	188	8.8	423	22	AAZ02899	DNA encoding human
41	188	8.8	423	22	AAZ02900	DNA encoding human
42	185.4	8.6	1404	19	AAZ01310	cDNA encoding rat
43	181.6	8.5	1450	20	AAZ80215	Mouse nuclear rece
44	172.2	8.0	1280	18	AAZ192305	Constitutively act
45	170.6	7.9	1450	14	AAZ46131	Human CAR receptor

ALIGNMENTS

RESULT 1	
AAZ07997	
ID	AAZ07997 standard; DNA: 2146 bp.
AC	AAZ07997:
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OT	17-JAN-2000 (first entry)
XX	
DE	Human pregnane X receptor (hpxr) encoding DNA.
XX	
XX	Human; nuclear receptor; pregnane X receptor; PXR; CYP: CYP3A4;
KW	cytochrome P-450 mono-oxygenase; drug interaction; hpxr; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0944815-A1.
XX	
PD	30-SEP-1999.
XX	
PF	26-MAR-1999; 99WD-US06737.
XX	
PR	27-MAR-1998; 98US-0079594.
XX	
XX	(GLAX) GLAXO GROUP LTD.
PA	
XX	
P1	Kilower SA, Willison TM;
XX	
DR	WPI: 1999-601202/51.
XX	P-RSDR: AAZ42691.
XX	
PT	New human pregnane X receptor, used to identify specific modulators and
XX	agents that induce expression of cytochrome P-450 mono-oxygenase
PS	Claim 4; Fig 1A-D; 69pp; English.


```

UY 1921 aatccctcagatcccaataatgtcgaatgttgaagaagacacagacacgaatgaag 1980
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DB 1921 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1980
UY 1981 ccaatcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2040
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DB 1981 ccaatcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2040
UY 2041 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2100
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DB 2041 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2100
UY 2101 taagctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2146
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DB 2101 taagctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 2146

RESULT 2
ID AAX59975 standard: DNA: 3057 BP.
XX
AC AAX59975:
XX
DI 04-AUG-1999 (first entry)
XX
DE DNA encoding an intranuclear receptor protein.
XX
KW Human: intranuclear receptor protein; drug development; diagnosis;
KM treatment; ss.
XX
OS Homo sapiens.
XX
PN JP1127872-A.
XX
PD 18-MAY-1999.
XX
PE 07-AUG-1998: 98JP-0224172.
XX
PR 11-AUG-1997: 97JP-0230435.
XX
PA (NISH ) JAPAN TOHACCO INC.
DB WPI: 1999-450340/40.
DR P-PSDB: AAY16045.
XX
PI New intranuclear receptor protein - useful for drug development and
PI diagnosis and treatment of disease
XX
PS Claim 10: Page 35-37; 38pp; Japanese.
XX
CC The present sequence encodes a human intranuclear receptor protein.
CC The nucleic acid sequence was isolated from a human adult cDNA
CC library using a swedish ANO24 derived probe. The protein can
CC be used for the development of drugs and diagnosis and treatment
CC of various diseases.
XX
XX
Sequence 3057 BP: 792 A: 751 C: 813 G: 701 T: 0 other:

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Query Match 98.6% Score 2115.4: DB 20: Length 3057:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 2116: Conservative 0: Mismatches 1: Gaps 0:

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DB 121 taagctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 180
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UY 210 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 269
      |||||||
DB 181 gatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 240
      |||||||
UY 270 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 429
      |||||||
DB 241 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 400
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UY 330 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 389
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DB 330 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 460
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UY 390 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 449
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DB 361 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 420
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UY 450 taagctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 509
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DB 421 taagctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 480
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UY 510 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 569
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DB 481 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 540
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UY 570 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 629
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DB 541 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 600
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UY 630 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 689
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DB 601 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 660
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DB 661 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 720
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DB 721 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 780
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DB 781 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 840
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DB 841 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 900
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UY 930 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 989
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DB 901 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 960
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UY 990 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1049
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DB 961 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1020
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UY 1050 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1109
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DB 1021 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1080
      |||||||
UY 1110 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1169
      |||||||
DB 1081 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1140
      |||||||
UY 1170 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1229
      |||||||
DB 1141 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1200
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UY 1230 aatccctcagatcccaataatgtcgaatgttgaagaagacacacgaacgaatgaag 1289
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[illegible][illegible]

Db 472 aatctcgaagctccccaatctcgcgtatattgagagaaagccactgcatctactca 531
 Uy 464 atctctatgacatgtaagatgcaagacattctcagagagacatgaaacgaagccc 523
 Db 532 atctctatgacatgtaagatgcaagacattctcagagagacatgaaacgaagccc 591
 Uy 524 ggcctgaagatgcccctccgaagagcctcgaatcaaccggaagacccagacat 583
 Db 592 ggcctgaagatgcccctccgaagagcctcgaatcaaccggaagacccagacat 651
 Uy 584 ggcctgaagatgcccctccgaagagcctcgaatcaaccggaagacccagacat 643
 Db 652 ggcctgaagatgcccctccgaagagcctcgaatcaaccggaagacccagacat 711
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 Db 712 cccgaacagccctgagagagagagagagagagagagagagagagagagagag 771
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 Uy 764 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 823
 Db 832 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 891
 Uy 824 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 883
 Db 892 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 951
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 Db 952 aagaaagctccgaag 1011
 Uy 944 agctcgaag 1003
 Db 1012 agctcgaag 1071
 Uy 1004 aagaaagctccgaag 1063
 Db 1072 aagaaagctccgaag 1131
 Uy 1064 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1123
 Db 1132 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1191
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 Db 1192 cccctcgaag 1251
 Uy 1184 cccctcgaag 1243
 Db 1252 cccctcgaag 1311
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 Db 1372 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1431
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 Db 1432 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1491
 Uy 1424 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1483
 Db 1492 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1551
 Uy 1484 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1543
 Db 1552 ggcctcagccactggaagagagagagagagagagagagagagagagagagagag 1611

Uy 1544 tccgaag 1604
 Db 1612 tccgaag 1671
 Uy 1604 ggcctcagccactggaag 1664
 Db 1672 ggcctcagccactggaag 1731
 Uy 1664 ggcctcagccactggaag 1723
 Db 1732 ggcctcagccactggaag 1791
 Uy 1724 ggcctcagccactggaag 1784
 Db 1792 ggcctcagccactggaag 1851
 Uy 1784 ggcctcagccactggaag 1843
 Db 1852 ggcctcagccactggaag 1911
 Uy 1844 ggcctcagccactggaag 1903
 Db 1912 ggcctcagccactggaag 1971
 Uy 1904 ggcctcagccactggaag 1963
 Db 1972 ggcctcagccactggaag 2031
 Uy 1964 ggcctcagccactggaag 2023
 Db 2032 ggcctcagccactggaag 2091
 Uy 2024 ggcctcagccactggaag 2083
 Db 2092 ggcctcagccactggaag 2151
 Uy 2084 ggcctcagccactggaag 2143
 Db 2152 ggcctcagccactggaag 2211
 Uy 2144 ggcctcagccactggaag 2146
 Db 2212 ggcctcagccactggaag 2214

RESULT 4
 AAX56242
 ID AAX56242 standard; cDNA; 2910 BP.
 XX
 AAX56242:
 AC
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Human vitamin D receptor related gamma protein encoding cDNA.
 KW Human; vitamin D receptor related protein; VDR; obesity; diabetes;
 KW anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidemia;
 KW hypercholesterolemia; hyperlipoproteinemia; osteoporosis; tumor;
 KW hyperproliferative skin disorder; hyperthyroidism; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09919354-A1.
 XX
 PD 22-APR-1999.
 XX
 PE 31-AUG-1998; 98W0-SE01548.
 XX
 PR 31-MAR-1998; 98SE-0001148.
 PR 14-OCT-1997; 97SE-0003745.
 XX
 PA (PIR) PHARMACIA & UPJOHN AB.


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Db 1636 ctgaagccgacacccgagcaagatgagactgccaagaagcgaactcctgc 1695
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Uy 1719 tgaactgctccctgaagaaattccctgactatgacgtgaactgacctccgaagaagc 1778
|||
Db 1696 tgaactgctccctgaagaaattccctgactatgacgtgaactgacctccgaagaagc 1755
|||
Uy 1779 atgggtgcccctccaccccaattcattctgataagaaatgaagccagacatttaacgag 1838
|||||
Db 1756 atgggtgcccctccaccccaattcattctgataagaaatgaagccagacatttaacgag 1815
|||
Uy 1839 aaatgtaactgaactatgaactgaagccatcagaaggaagatgaccttccctttaa 1898
|||||
Db 1816 aaggtgtaactgaactatgaactgaagccatcagaaggaagatgaccttccctttaa 1875
|||
Uy 1899 aaggtgtaactgctcgaaggaagaaatccctctgatacccaataatgctcaagatgagaag 1958
|||||
Db 1876 aaggtgtaactgctcgaaggaagaaatccctctgatacccaataatgctcaagatgagaag 1935
|||
Uy 1959 gaacgaagcaacgaagaatgaagccatctgaactatgacacataaccacatttatg 2018
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Db 1936 gaacgaagcaacgaagaatgaagccatctgaactatgacacataaccacatttatg 1995
|||
Uy 2019 ctctctgaactcttctgaactgaactgaactgaactgaactgaactgaactgaactgaact 2078
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Db 1996 ctctctgaactcttctgaactgaactgaactgaactgaactgaactgaactgaactgaact 2055
|||
Uy 2079 ctctctctctgaactgcttctgaactgaactgaactgaactgaactgaactgaactgaact 2138
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Db 2056 ctctctctctgaactgcttctgaactgaactgaactgaactgaactgaactgaactgaact 2115
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Uy 2146 atctatg 2146
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Db 2116 atctatg 2123

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RESULT 5

AAK59974
ID AAK59974 Standard: UNK: 1243 BP.

AC AAK59974:

XX 04-AUG-1999 (first entry)

XX DNA encoding an intranuclear receptor protein.

XX Human: intranuclear receptor protein; drug development; diagnosis;

XX Treatment; ss.

XX Homo sapiens.

XX JP11127872-A.

XX 18-MAY-1999.

XX 07-AUG-1998: 98JP-0224172.

XX 11-AUG-1997: 97JP-0230335.

XX (NISR) JAPAN TOHOKU INC.

XX WPI: 1999-450310/40.

XX P-PSDB: AAY15936.

XX New intranuclear receptor protein - useful for drug development and

XX diagnosis and treatment of disease.

XX Claim 10: Page 32-35; 38pp; Japanese.

XX The present sequence encodes a human intranuclear receptor protein.

XX The nucleic acid sequence was isolated from a human adult cDNA

XX library using a well-known AMO23 derived probe. The protein can

XX be used for the development of drugs and diagnosis and treatment

CC of various diseases.

XX Sequence 3243 BP: 838 A: 806 C: 862 G: 747 T: 0 other:

Query Match 94.58: Score 2006.4: DB 20: Length 4241:

Best Local Similarity 94.38: P-Seq No. 0:

Matches 2145: Conservative 0: Mismatches 1: Indels 128: Gaps 1:

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Uy 1 tgaatataagatgaaagaaagatttatctatctcgaagaaatcaataaactatgaatga 60
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Db 30 tgaatataagatgaaagaaagatttatctatctcgaagaaatcaataaactatgaatga 89
|||
Uy 61 gacgagaaagaaagaaagactgaccttgaactgaatgaagatctcgaactgaactgaagac 120
|||
Db 90 gacgagaaagaaagaaagactgaccttgaactgaatgaagatctcgaactgaactgaagac 149
|||
Uy 121 aagatgtaactgaagaaagaaagaaagaaatgaagatgaactgaactgaactgaagaaagaa 180
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Db 150 aagatgtaactgaagaaagaaagaaagaaatgaagatgaactgaactgaactgaagaaagaa 209
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Uy 181 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 240
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Db 210 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 269
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Uy 241 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 281
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Db 270 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 329
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Uy 282 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 281
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Db 330 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 389
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Uy 282 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 292
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Db 390 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 449
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Uy 293 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 452
|||||
Db 450 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 509
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Uy 453 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 412
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Db 510 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 569
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Uy 413 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 472
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Db 570 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 629
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Uy 473 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 542
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Db 630 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 689
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Uy 533 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 592
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Db 690 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 749
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Uy 593 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 652
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Db 750 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 809
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Db 870 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 929
|||
Uy 773 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 842
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Db 930 ctgctctctgaatgaagaaactgaactgaactgaactgaactgaactgaactgaactgaact 989

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[illegible][illegible]

[illegible][illegible]

XX Sequence 2068 bp: 520 A: 541 C: 586 G: 420 T: 1 other:

Query Match: 81.4%; Score 1744.4; DB 22; Length 2068;
 Post Local Similarity 99.4%; Pred. No. 0;
 Matches 1781; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

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UY 1 taaatataatgaagagagagatttctcatalatccggagaaatcaataactatgaatag 60
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Db 280 taaatataatgaagagagagagatttctcatalatccggagaaatcaataactatgaatag 339
UY 61 gacgagaaagaaagacactgcttacttcaatggagatctgagctcagctctgaagcc 120
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Db 340 gacgagaaagaaagacactgcttacttcaatggagatctgagctcagctctgaagcc 399
UY 121 aagttcttcaatgaagaaagagaaatagatcaatcaactgctctcgaacagagag 180
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Db 400 aagttcttcaatgaagaaagagaaatagatcaatcaactgctctcgaacagagag 459
UY 181 cagatctcttgaatgaagctatcttcttgaatgcatcttgcacccagatggttcaaatgagac 240
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Db 460 cagatctcttgaatgaagctatcttcttgaatgcatcttgcacccagatggttcaaatgagac 519
UY 241 ccccaagagagagatcagagcaaaagacttaccacaaagcaatccaaagagcccaagaca 300
    |||||||
Db 520 ccccaagagagagatcagagcaaaagacttaccacaaagcaatccaaagagcccaagaca 579
UY 301 aaacttgaagtagagaccccaaaagacttgaagacatgctgacttctgacatgaagac 360
    |||||||
Db 580 aaacttgaagtagagaccccaaaagacttgaagacatgctgacttctgacatgaagac 639
UY 361 acagatctgcttctcgaagaaacccatgttcaacagagatgaagagtcgagagtcacca 420
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Db 640 acagatctgcttctcgaagaaacccatgttcaacagagatgaagagtcgagagtcacca 699
UY 421 atcttcagatgcatgttgaagaaagagccctgagatgcatgcatgcatgcatgcatgcat 480
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Db 700 atcttcagatgcatgttgaagaaagagccctgagatgcatgcatgcatgcatgcatgcat 759
UY 481 gcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 540
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Db 760 gcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 819
UY 541 cagaaagagcgttcttgcagaaaccccaagagaccccaagagatgccaagctgcccctg 600
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Db 820 cagaaagagcgttcttgcagaaaccccaagagaccccaagagatgccaagctgcccctg 879
UY 601 cagaaagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 660
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Db 880 cagaaagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 939
UY 661 gagaaagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 720
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Db 740 gagaaagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 999
UY 741 gtagagagagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 780
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Db 1000 gtagagagagcgttcttgcagaaaccccaagagagatgcatgcatgcatgcatgcatgcatgcat 1059
UY 781 aaacatcttgaacatcacttccatcttcaagaaatctccagcttgcagagctgcttagc 840
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Db 1060 aaacatcttgaacatcacttccatcttcaagaaatctccagcttgcagagctgcttagc 1119
UY 841 aatgagcttgcagatctcagaaatcttgcagagcccatcagagaaagaaatctcagaaatg 900
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Db 1120 aatgagcttgcagatctcagaaatcttgcagagcccatcagagaaagaaatctcagaaatg 1179
UY 901 aagcagagtcagaaagaaatctcagatcttgcagagctctctgcagagtcagagagagag 959
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Db 1180 aagcagagtcagaaagaaatctcagatcttgcagagctctctgcagagtcagagagagag 1239
UY 960 tggagagtcagagaaatcaaaaccccaagcagagtcagagagagagaaatcttctctct 1019
  
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Db 1240 tggagagtcagagaaatcaaaaccccaagcagagtcagagagagagaaatcttctctct 1298
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Db 1299 gctgcacacatgagatgagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1358
UY 1080 agtcatcttcttacttgcagagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1139
    |||||||
Db 1359 agtcatcttcttacttgcagagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1418
UY 1140 cagcttcaaatgtgttcaaatgagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1199
    |||||||
Db 1419 cagcttcaaatgtgttcaaatgagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1478
UY 1200 ggaatgtgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1259
    |||||||
Db 1479 ggaatgtgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1538
UY 1260 actgagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1319
    |||||||
Db 1539 actgagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1598
UY 1320 atagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1379
    |||||||
Db 1599 atagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1658
UY 1380 cccagagatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1439
    |||||||
Db 1659 cccagagatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1718
UY 1440 caatcagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1499
    |||||||
Db 1719 caatcagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1778
UY 1500 gctgcagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1559
    |||||||
Db 1779 gctgcagagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1838
UY 1560 ctttgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1619
    |||||||
Db 1839 ctttgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1898
UY 1620 tgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1679
    |||||||
Db 1898 tgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1957
UY 1680 aagacagatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1739
    |||||||
Db 1958 aagacagatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 2017
UY 1740 tcttgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 1790
    |||||||
Db 2018 tcttgaatgagcagatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 2068
  
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HK5011.10
 AAX59967
 ID AAX59967 standard; DNA: 1774 bp.
 AC AAX59967;
 DT 04-AUG-1999 (first entry)
 DX
 DE DNA encoding an intracellular receptor protein.
 KW Human: intracellular receptor protein; drug development; diagnosis;
 treatment; SS.
 KM
 OS Homo sapiens.
 XX
 FN J01127872-A.
 XX

claim 4, page 22, 23, 44pp; Japanese.

XX The present sequence encodes a human interleukin receptor protein.
XX The nucleic acid sequence was isolated from a human adult cDNA
XX library using a well known AMO4 derived probe. The probe can
XX be used for the development of drugs and diagnostics and treatment
XX of various diseases.

XX Sequence: 1005 BP; 304 A; 456 C; 486 G; 209 T; 0 other.

Query Match: 60, 80%; Score: 1405; Len: 20; Length: 1005;

Insert: Insert: 100, 0%; Prob: No; 0;

Matches: 100%; Conserved: 0; Mismatch: 0; Indels: 0; Gaps: 0;

001 002 003 004 005 006 007 008 009 010 011 012 013 014 015 016 017 018 019 020 021 022 023 024 025 026 027 028 029 030 031 032 033 034 035 036 037 038 039 040 041 042 043 044 045 046 047 048 049 050 051 052 053 054 055 056 057 058 059 060 061 062 063 064 065 066 067 068 069 070 071 072 073 074 075 076 077 078 079 080 081 082 083 084 085 086 087 088 089 090 091 092 093 094 095 096 097 098 099 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

001 002 003 004 005 006 007 008 009 010 011 012 013 014 015 016 017 018 019 020 021 022 023 024 025 026 027 028 029 030 031 032 033 034 035 036 037 038 039 040 041 042 043 044 045 046 047 048 049 050 051 052 053 054 055 056 057 058 059 060 061 062 063 064 065 066 067 068 069 070 071 072 073 074 075 076 077 078 079 080 081 082 083 084 085 086 087 088 089 090 091 092 093 094 095 096 097 098 099 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

XX The present invention relates to a composition comprising several

XX polynucleotide probes. Probes can be derived from the present sequence,

XX the probes are immobilised and are preferably useful as hybridisable

XX array elements in a microarray for monitoring the expression of several

XX polynucleotides. The microarray can be used in the diagnosis of cancers

XX such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma

CC and testicular carcinoma etc., immunopathology such as AIDS, Addison's
 CC disease, adult respiratory distress syndrome, allergies, anemia, asthma,
 CC or scleroderma and bronchitis etc., neuropathology such as Alzheimer's
 CC disease, amyotrophic lateral sclerosis, bipolar disorder,
 CC cataplexy and cerebral neoplasms etc. The microarray can also be used to
 CC investigate an individual's predisposition to a disease such as cancer,
 CC immunopathology or neuropathology. Also, the microarray can be used for
 CC investigating cellular response to infection, drug treatment etc. The
 CC microarray can be used for diagnostics, prognosis and treatment
 CC requirements, drug discovery and development, toxicological and
 CC carcinogenicity studies, forensics, pharmacogenomics etc. The array can
 CC also be used for monitoring disease progression.

XX
 XX
 Sequence 801 BP; 200 A; 199 C; 258 G; 143 T; 1 other;

Query Match 44.3%; Score 716.6; DB 22; Length 801;
 Best Local Similarity 98.2%; Pred. No. 2,56-181;
 Matches 776; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

UY 170 gaacaaagacagagagctcttgaataagcttactcttgaatcactcttgaacagagatagt 229
 DB 13 gaacaaagacagagagctcttgaataagcttactcttgaatcactcttgaacagagatagt 72
 UY 240 tcaaatgaaccccaagagagagagctcgaagcaaaagcttaccacacagagctcgaag 289
 DB 74 tcaaatgaaccccaagagagagagctcgaagcaaaagcttaccacacagagctcgaag 132
 UY 290 gcccagaagcaaaccttgaagagcttgaaccccaagagagcttgaacagagcttgaac 349
 DB 133 gcccagaagcaaaccttgaagagcttgaaccccaagagagcttgaacagagcttgaac 192
 UY 350 actctgaagacacagagcttgaatcctcgaagacccagagcttgaacagagagagag 409
 DB 193 actctgaagacacagagcttgaatcctcgaagacccagagcttgaacagagagagag 252
 UY 410 gaggagcccaaatctcctctatcttgaagagagagagagagagagagagagagagag 469
 DB 253 gaggagcccaaatctcctctatcttgaagagagagagagagagagagagagagagag 312
 UY 470 taactgttaag 529
 DB 313 taactgttaag 372
 UY 530 gattcctcttccgaag 589
 DB 373 gattcctcttccgaag 432
 UY 590 cctcag 649
 DB 433 cctcag 492
 UY 650 gctcag 709
 DB 494 gctcag 552
 UY 710 aagcag 769
 DB 553 aagcag 612
 UY 770 agcag 827
 DB 613 agcag 672
 UY 828 aagcag 886
 DB 673 aagcag 732
 UY 887 aagcag 946
 DB 743 aagcag 791
 UY 947 tgcag

DB 792 tgcag

RESULT 14
 AAX59972
 ID AAX59972 standard; DNA: 644 BP.

XX AAX59972:

XX 04-AUG-1999 (first entry)

XX SEQ ID 12 of JP11127872.

XX Human: intranuclear receptor protein; drug development; diagnostics;

XX treatment; ss.

XX Homo sapiens.

XX JP11127872-A.

XX 18-MAY 1999.

XX 07-AUG-1998: 98JP-0224172.

XX 11-AUG-1997: 97JP-0230345.

XX (NIBS) JAPAN T-BMW INC.

XX WPI: 1999-350330/40.

XX New intranuclear receptor protein - useful for drug development and

XX diagnosis and treatment of disease

XX Disclosure; Page 32; 38pp; Japanese.

XX The specification describes a human intranuclear receptor protein.

XX The nucleic acid sequence was isolated from a human adult cDNA

XX library using a swedish ANO23 derived probe. The protein can

XX be used for the development of drugs and diagnosis and treatment

XX of various diseases. The present sequence was used in the course of

XX the invention.

Sequence 644 BP; 175 A; 161 C; 193 G; 115 T; 0 other;

Query Match 28.3%; Score 608.2; DB 20; Length 644;
 Best Local Similarity 99.4%; Pred. No. 4,76-148;
 Matches 621; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

UY 79 taacttacttgaatgag 148
 DB 12 taacttacttgaatgag 70
 UY 139 aagcag 198
 DB 71 aagcag 140
 UY 199 actccttacttgaatgag 258
 DB 131 actccttacttgaatgag 190
 UY 259 gcaaaag 318
 DB 191 gcaaaag 250
 UY 319 aagcag 378
 DB 251 aagcag 310
 UY 379 aagcag 438
 DB 311 aagcag 370

[illegible]

```

: RESULT 3
: US-07-747-7468-5
: Sequence 5, Application US/0773736B
: Patent No. 5260199
:
: GENERAL INFORMATION:
:
: APPLICANT: Deluca, Hector F.
:
: APPLICANT: Ross, Troy K.
: APPLICANT: Prahl, Jean M.
:
: TITLE OF INVENTION: Method of producing
:
: NUMBER OF SEQUENCES: 6
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
:
: STREET: 411 East Wisconsin Avenue

```

```

1 CITY: Milwaukee
2 STATE: Wisconsin
3 COUNTRY: U.S.A.
4 ZIP: 53202
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent to Rolfe #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/07/37,736B
12 FILING DATE: 19910730
13 CLASSIFICATION: 435
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Schwartz, Carl R.
16 REGISTRATION NUMBER: 29,437
17 REFERENCE/DOCKET NUMBER: 96-296-2185-2
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 414-277-5715
20 TELEFAX: 414-277-5774
21 INFORMATION FOR SEQ ID NO: 5:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 1399 base pairs
24 TYPE: NUCLEIC ACID
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA
28 HYPOTHEetical: No
29 ANTI-SENSE: No
30 ORIGINAL SOURCE:
31 ORGANISM: Homo sapiens
32 PUBLICATION INFORMATION:
33 AUTHORS: Baker, Andrew R.
34 AUTHORS: McMonnell, Donald P.
35 AUTHORS: Hughes, Tracy
36 AUTHORS: Crisp, Tracey M.
37 AUTHORS: Mangelsdorf, David J.
38 AUTHORS: Haussler, Mark R.
39 AUTHORS: Pike, J. W.
40 AUTHORS: Shine, John
41 AUTHORS: O'Malley, Bert W.
42 TITLE: Cloning and expression of full-length cDNA
43 TITLE: encoding human vitamin D receptor
44 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
45 VOLUME: 85
46 PAGES: 3294-3298
47 DATE: May-1988
48 US-07-737-736B-5
49
50 Query Match 12-7% Score 272.8; DB 1; Length 1399;
51 Best Local Similarity 55-1%; Pred. No. 46-5%;
52 Matches 638; Conservative 0; Mismatches 487; Indels 34; Gaps 4;
53
54 QY 415 ccgcacatctgacctgtatcggaggaacaggccattcaactcaatcatgaca 474
55 ||| |||| | | |||| || | |||| |||| | |||| |||| | ||||
56 Db 176 ccccgatcttgccgcttctgtttgacacgccagccatctgcttaccattatgac 245
57
58 QY 475 tatgaagatctgaagagcttttttcagaagagccaataaaacagccagcttaaatgag 534
59 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
60 Db 236 tcttgaaagcttcgaanagctttctcaagccaacatctcaacccgaagccattatctactttgat 295
61
62 QY 535 ccccttcgaagagagagcctcagaagatcacctcgaagaatcccagagaaatcccaagccag 594
63 ||||| | | | | | ||||| ||||| | | | | | ||||| |||||
64 Db 296 cctcttc---AACGGGAGACTGCCGCATCTCAAGGGAACCTAAATGTCCATTGTCAAGTTCAG 452
65
66 QY 595 cctcttcgaagagagcctcagaagagcaatgaagagagatgatatcctcgaagagagc 654
67 ||| | | | | ||||| ||||| ||||| ||||| ||||| |||||
68 Db 353 cgcgctcaaaaacgttgttatgacattgacacatgataaagcattattttctcagatgacaaa 412
69
70 QY 655 atggagagagagagagccttgatcgaagcgaagaaatgaagcgaagagagagagatgagaga 714
71 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
72 Db 413 gtgcagagagagagagagatgattctgaaagtcgaaagcgaagagagagagagagagat 472

```


1

Genature version 4.5
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CM nucleotide - nucleotide search, using sw model

Run on: March 2, 2002, 00:44:29 ; Search time 1369.92 Seconds
(without alignments)
16833.422 Million cell updates/sec

Title: US-09-276-935b-13
Perfect score: 2146
Sequence: 1 tgaatataatgataatgatac.....aggtcctatgataatcctgaa 2146

Scoring table:
Gapop 10.0 ; Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : EST:

1: em_est1: *
2: em_est1: *
3: em_est1: *
4: em_est1: *
5: em_est1: *
6: em_est1: *
7: em_est1: *
8: em_est1: *
9: em_est1: *
10: em_est1: *
11: em_est1: *
12: em_est1: *
13: em_est1: *
14: em_est1: *
15: em_est1: *
16: em_est1: *
17: em_est1: *
18: em_est1: *
19: em_est1: *
20: em_est1: *
21: em_est1: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1006.8	46.9	2525	AK018630	Mus muscu
2	430.6	20.1	489	B1252289	602953007
3	370.8	17.3	794	A1746915	u109a10.y
4	343.6	16.0	399	B6955533	C64-CT065
5	343	16.0	343	A1248626	q677b12.x
6	325.4	15.2	677	AK011108	Mus muscu
7	288.8	13.5	300	A0099521	A0099521
8	222	10.3	638	AV651714	AV651714
9	214.8	10.0	454	N94132	2a25406.f1
10	201	9.4	472	AA27370	va81a12.f
11	199.6	9.3	493	AA871811	da94c06.y
12	185.4	8.6	200	AA679591	z349d12.s

13	177.6	8.3	837	10	AA140214
14	166.4	7.8	463	10	AA511148
15	165.4	7.7	215	10	AA108557
16	159.6	7.4	677	11	BF788461
17	158	7.4	689	11	BF577692
18	156.8	7.3	432	10	AA158294
19	154.4	7.2	601	10	AA107536
20	147	6.8	776	11	BF686868
21	143.8	6.7	560	10	AA1768052
22	141.6	6.6	654	11	BF102347
23	140.8	6.6	1053	10	BF573696
24	140.4	6.5	806	13	AZ716452
25	140.2	6.5	835	11	BF159453
26	136	6.3	734	11	BF686272
27	132.8	6.2	540	10	AA012320
28	132	6.2	463	10	AA1049299
29	127.6	5.9	748	11	BF694682
30	124.6	5.8	832	11	BF565979
31	118	5.5	724	10	AA1046425
32	116.6	5.4	519	11	BF1029636
33	116.2	5.4	391	13	AZ816919
34	108.4	5.1	468	10	AA396982
35	103.6	4.8	950	10	AA155996
36	103.4	4.8	778	11	BF383394
37	102	4.8	463	10	AA107961
38	101.6	4.7	859	10	AA152278
39	101.2	4.7	506	10	AA679391
40	100.8	4.7	616	10	AA128347
41	100.8	4.7	859	10	AA1583005
42	99.6	4.6	683	11	BF783185
43	99.2	4.6	732	10	AA393915
44	99	4.6	370	10	AA1024672
45	99	4.6	507	10	AA264990

ALIGNMENTS

RESULT 1	AK018630	2525 bp	mRNA	HTC	05-JUL-2001
LOCUS	Mus musculus adult male cecum cDNA, RIKEN full-length cDNA				
DEFINITION	AK018630	2525 bp	mRNA	HTC	05-JUL-2001
ACCESSION	AK018630	2525 bp	mRNA	HTC	05-JUL-2001
VERSION	AK018630.1	GI:12858444			
KEYWORDS	CDP triphosphatase				
SOURCE	Mus musculus (strain: C57BL/6J) adult male cecum cDNA to mRNA, clone: F10010118.				
ORGANISM	Mus musculus				
REFERENCE	Enkayola, M.; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 2525)				
TITLE	Carnitine, P., and Hayashizaki, Y.				
JOURNAL	High efficiency full length cDNA cloning				
MEDLINE	Methods in enzymology, 303, 19-44 (1999)				
PubMed	99279253				
REFERENCE	10349636				
AUTHORS	2 (bases 1 to 2525)				
TITLE	Carnitine, P., Shihata, Y., Hayashi, N., Shihata, K.,				
JOURNAL	Shihata, K., Itoh, M., Aizawa, K., Nagata, S., Sasaki, N., Carnitine, P.,				
MEDLINE	Kono, H., Akiyama, D., Nishikawa, K., Kishimoto, T., Tashiro, H., Itoh, M.,				
PubMed	Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishio, T., Harada, A.,				
REFERENCE	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikeda, T., Kashiwagi, K.,				
AUTHORS	Fujikawa, S., Iino, K., Touda, Y., Iwano, M., Ohara, E., Watabiki, M.,				
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawada, T.,				

DB	1186	1223	1246	QY	1283	DB	1306	QY	1343	DB	1366	QY	1403	DB	1426	QY	1463	DB	1486	QY	1523	DB	1546	QY	1583	DB	1606	QY	1643	DB	1666	QY	1703	DB	1724		
NCBI	U000000000	U000000000	U000000000	U000000000	U000000000	NCBI	U000000000	U000000000	U000000000	NCBI	U000000000	U000000000	U000000000	U000000000	NCBI	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000	U000000000		
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						
1245	1245	1245	1305	1342	1365	1425	1485	1502	1545	1582	1605	1642	1665	1702	1723																						

	/Library_*	*Issue_Type "hepatocellular carcinoma, cell line"			
	/Lib_host =FDH10B (phage-resistant)				
	/Host_Organism:	Liver; Vector: pOH7; Site_L1: XhoI; Site_L2: EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGGAG(G). Size-selected ~500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II-MJ (Life Technologies). Note: This is a NIH_MGC			
BASE COUNT	142 a	118 c	136 g	93 t	
ORIGIN					
Query Match:	Best Local Similarity	20.1%	Score 430.6;	Dh_H:	Length 489;
Matches	473;	Conservative	0;	Mismatch	9;
				Indels	7;
				Gaps	4;
OY	64 ggagaaggaaagactgaccttctacgc-ggggaattcgaqccgaqqccaqaatca	122			
IDb	1 GGAAGAAGCAACACTGCCCTTAATTACATCCGAAATCCTAACCCTCATGTTCACAACATAA	60			
OY	123 gtgttcctcatgtagaaaaccgaagaaataaacataactgccctgtcccctaacaacatcg	182			
IDb	61 GTTTTGACAGTAGAAAAAACAAAAGCAATTAAGCTAACTGCTCTCAAAGAAAGAGAG	120			
OY	183 gctcccttaataaagtctactctctaatgatgaccttttgacacgaatatcataatgacac	242			
IDb	121 GCTCCTTGSIAAAGCTACGCTCTTAATGCATGCTTTGCAAGCGGATTTGTTAAAGTGAATCC	180			
OY	243 gagggagagaaatcgaagaccaaagaacttacaccaaaagaaatccccaaagcccgaagaa	302			
IDb	181 CAGGGAGACAGCTGGGAGCCAAGCAACTTACACCAAGCACAGTCCAAAGAGGCCCAAGCAAA	240			
OY	303 ctctgaagatgaagaccgaagaaagctctgaagacat--gctgaaccttgtgaactgaagac	360			
IDb	241 CCTGGAGGTGAGAACCCCAGAAAGAGCTGGAGGCATATAGCTTTTTGTATNTGTGAGAGAC	300			
OY	361 acagaagctgttctctggaagaccgaatcacagcgaatgaagaaatcgaagatccccaa	420			
IDb	301 ACAGATCTGTTGCTGGAAAGCCCCAGATGCAAGCAATGCAAGAAATGCGAAATCTCTCA	360			
OY	421 atctacgcttatataaaaa-----gcaagagcgaatgaqtatgcccttgcataaagatg	476			
IDb	361 ATCTSCCGTGATGTGAGGAGCAACAAAAGGCVAA'TGCTATVAA'TTCAATGATATGACATG	420			
OY	477 tgaaagdaatcgaaggaatcttlctcagaagaaatcaaacacgaagcccaatgaagatgac	536			
IDb	421 TGAATATATCAAGAGGATTTTTCAGAGAGGCGCATGAAATGTAATGCGAGATGABRRTGTC	480			
OY	537 ctctccgaaa ga5				
IDb	481 CTTCGGCA 489				
RESULT	3				
AUTOGUENES	A1746915	794 bp	mRNA	EST	22-NOV-1999
DEFINITION	Unigenes.Lv1 Snailin mouse embryo mwa Mus musculus cDNA clone IMAGE:257262.5 similar to U1054915 c54915 PREMANE-X REF:PT-H, .. mRNA sequence.				
ACCESSION	A1746915				
VERSION	A1746915.1 GI:5125179				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Fukayama J Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Euarchia: Rodentia: Scurionathii: Muridae: Murinae: Mus. 1 (bases 1 to 794)				
AUTHORS	Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,F., Underwood,K., Skopron,M., Thelston,B., Allen,M., Howars,Y., Person .B., Waller.T., Gibbons.M, Page.D., Harvey.N., Schork.R., Rutter				

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